

134

TTC GAC AAG CCC TAT CTG CTC GCG ATG GCC AAC GCC GGT CCG GGC ACC Phe Asp Lys Pro Tyr Leu Leu Ala Met Ala Asn Ala Gly Pro Gly Thr 100 105 110 115	566
AAC GGC TCA CAG TTT TTC ATC ACC GTC GGC AAG ACT CCG CAC CTG AAC Asn Gly Ser Gln Phe Phe Ile Thr Val Gly Lys Thr Pro His Leu Asn 120 125 130	514
CGG CGC CAC ACC ATT TTC GGT GAA GTG ATC GAC GCG GAG TCA CAG CGG Arg Arg His Thr Ile Phe Gly Glu Val Ile Asp Ala Glu Ser Gln Arg 135 140 145	662
GTT GTG GAG GCG ATC TCC AAG ACG GCC ACC GAC GGC AAC GAT CGG CCG Val Val Glu Ala Ile Ser Lys Thr Ala Thr Asp Gly Asn Asp Arg Pro 150 155 160	710
ACG GAC CCG GTG GTG ATC GAG TCG ATC ACC ATC TCC TGA CCGAAGCTA Thr Asp Pro Val Val Ile Glu Ser Ile Thr Ile Ser 165 170 175	759
GGTGGCTCG TCGTCGAAT ACACCTTGTG GACCGGCCAG GGCACGTGGC GGTACACCGA 819	
CACGCCGTG GGGCGGTTCA ACCGAGACGCC CTCACGCCAA GTCCGCTCAC CTITGGCCGC 879	
GACCGGCTTA ACCCGCAGCG GTAAGCGCAT CGAGCACCTC CACTGGGTG GTCCGAGAT 939	
CCGACGGGA 949	

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 182 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Met Ala Asp Cys Asp Ser Val Thr Asn Ser Pro Leu Ala Thr Ala Thr -7 -5 1 5
Ala Thr Leu His Thr Asn Arg Gly Asp Ile Lys Ile Ala Leu Phe Gly 10 15 20 25
Asn His Ala Pro Lys Thr Val Ala Asn Phe Val Gly Leu Ala Gln Gly 30 35 40
Thr Lys Asp Tyr Ser Thr Gln Asn Ala Ser Gly Gly Pro Ser Gly Pro 45 50 55
Phe Tyr Asp Gly Ala Val Phe His Arg Val Ile Gln Gly Phe Met Ile 60 65 70
Gln Gly Gly Asp Pro Thr Gly Thr Gly Arg Gly Gly Pro Gly Tyr Lys 75 80 85

135

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Phe Ala Asp Glu Phe His Pro Glu Leu Gln Phe Asp Lys Pro Tyr Leu
 90                      95                      100                      105

Leu Ala Met Ala Asn Ala Gly Pro Gly Thr Asn Gly Ser Gln Phe Phe
110                      115                      120

Ile Thr Val Gly Lys Thr Pro His Leu Asn Arg Arg His Thr Ile Phe
125                      130                      135

Gly Glu Val Ile Asp Ala Glu Ser Gln Arg Val Val Glu Ala Ile Ser
140                      145                      150

Lys Thr Ala Thr Asp Gly Asn Asp Arg Pro Thr Asp Pro Val Val Ile
155                      160                      165

Glu Ser Ile Thr Ile Ser
170                      175

```

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1060 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium tuberculosis*
- (B) STRAIN: H37Rv

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 201..860

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 201..295

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 297..860

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

```

TGGACCTTCA CGGCGGTCC CTTCGCTTCG GGGCGGACAC CTAACATCTT GGTGCTCACC      60
CTACCGCGAC ACCGCTGGGA CTTTGTGCGA TTGCGGGGCA CTCGGGGCGG CTGCGGGCTG      120
GAAATATGGT TGGGCGACGG GCGGCCGCGG GTCGCTACCA TCCCACTGTG AATGATTTAC      180
TGACCCGCGG ACTGCTCACC ATG GGC GCG GCC GCC GCA ATG CTG GCC GCG      230
          Met Gly Ala Ala Ala Ala Met Leu Ala Ala
          -32      -30      -25

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136

GTG CTT CTG CTT ACT CCC ATC ACC GTT CCC GGC GGC TAC CCC GGT GCC	278
Val Leu Leu Leu Thr Pro Ile Thr Val Pro Ala Gly Tyr Pro Gly Ala	
-28 -15 -10	
GTT GCA CCG GCC ACT GCA GCC TGC CCC GAC GCC GAA GTG GTG TTC GCC	326
Val Ala Pro Ala Thr Ala Ala Cys Pro Asp Ala Glu Val Val Phe Ala	
-5 1 5 10	
CGC GGC CGC TTC GAA CCG CCC GGG ATT GGC ACG GTC GGC AAC GCA TTC	374
Arg Gly Arg Phe Glu Pro Pro Gly Ile Gly Thr Val Gly Asn Ala Phe	
15 20 25	
GTC AGC GCG CTG CGC TCG AAG GTC AAC AAG AAT GTC GGC GTC TAC GCG	422
Val Ser Ala Leu Arg Ser Lys Val Asn Lys Asn Val Gly Val Tyr Ala	
30 35 40	
GTG AAA TAC CCC GCC GAC AAT CAG ATC GAT GTG GGC GCC AAC GAC ATG	470
Val Lys Tyr Pro Ala Asp Asn Gln Ile Asp Val Gly Ala Asn Asp Met	
45 50 55	
AGC GCC GAC ATT CAG AGC ATG GCC AAC AGC TGT CCG AAT ACC CGC CTG	518
Ser Ala His Ile Gln Ser Met Ala Asn Ser Cys Pro Asn Thr Arg Leu	
60 65 70	
GTG CCC GGC GGT TAC TCG CTG GGC GCG GCC GTC ACC GAC GTG GTA CTC	566
Val Pro Gly Gly Tyr Ser Leu Gly Ala Ala Val Thr Asp Val Val Leu	
75 80 85 90	
GCG GTG CCC ACC CAG ATG TGG GGC TTC ACC AAT CCC CTG CCT CCC GGC	614
Ala Val Pro Thr Gln Met Trp Gly Phe Thr Asn Pro Leu Pro Pro Gly	
95 100 105	
AGT GAT GAG CAC ATC GCC GCG GTC GCG CTG TTC GGC AAT GGC AGT CAG	662
Ser Asp Glu His Ile Ala Ala Val Ala Leu Phe Gly Asn Gly Ser Gln	
110 115 120	
TGG GTC GGC CCC ATC ACC AAC TTC AGC CCC GGC TAC AAC GAT CGG ACC	710
Trp Val Gly Pro Ile Thr Asn Phe Ser Pro Ala Tyr Asn Asp Arg Thr	
125 130 135	
ATC GAG TTG TGT CAC GGC GAC GAC CCC GTC TGC CAC CTT GCC GAC CCC	758
Ile Glu Leu Cys His Gly Asp Asp Pro Val Cys His Pro Ala Asp Pro	
140 145 150	
AAC ACC TGG GAG GCC AAC TGG CCC CAG CAC CTC GCC GGG GCC TAT GTC	806
Asn Thr Trp Glu Ala Asn Trp Pro Gln His Leu Ala Gly Ala Tyr Val	
155 160 165 170	
TGG TGG GGC ATG GTC AAC CAG GCG GCT GAC TTC GTT GCC GGA AAG CTG	854
Ser Ser Gly Met Val Asn Gln Ala Ala Asp Phe Val Ala Gly Lys Leu	
175 180 185	
CAG TAG CCACCTAGCC CCGCGCGSAG TCTTTGCTTC AGCGTTTGGC TAACCGACCA	910
Gln	
ACGCGCGCAC GATGAGGGGG TCGTGGTCA TATCAAGACA AGAAGGGAGT AGCGGATGCA	970

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CGCAAAAGTC GCGACTACC TCGTGGTGA GGCACACACC ACCGAACGGC ATGATCAACR 1030
 TGCTGAGATC ATCGAGGTGC GCTCCGACAA 1060

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Met Gly Ala Ala Ala Met Leu Ala Ala Val Leu Leu Thr Pro
 -32 -30 -25 -20
 Ile Thr Val Pro Ala Gly Tyr Pro Gly Ala Val Ala Pro Ala Thr Ala
 -15 -10 -5
 Ala Cys Pro Asp Ala Glu Val Val Phe Ala Arg Gly Arg Phe Gln Pro
 1 5 10 15
 Pro Gly Ile Gly Thr Val Gly Asn Ala Phe Val Ser Ala Leu Arg Ser
 20 25 30
 Lys Val Asn Lys Asn Val Gly Val Tyr Ala Val Lys Tyr Pro Ala Asp
 35 40 45
 Asn Gln Ile Asp Val Gly Ala Asn Asp Met Ser Ala His Ile Gln Ser
 50 55 60
 Met Ala Asn Ser Cys Pro Asn Thr Arg Leu Val Pro Gly Gly Tyr Ser
 65 70 75 80
 Leu Gly Ala Ala Val Thr Asp Val Val Leu Ala Val Pro Thr Gln Met
 85 90 95
 Trp Gly Phe Thr Asn Pro Leu Pro Pro Gly Ser Asp Gln His Ile Ala
 100 105 110
 Ala Val Ala Leu Phe Gly Asn Gly Ser Gln Trp Val Gly Pro Ile Thr
 115 120 125
 Asn Phe Ser Pro Ala Tyr Asn Asp Arg Thr Ile Glu Leu Cys His Gly
 130 135 140
 Asp Asp Pro Val Cys His Pro Ala Asp Pro Asn Thr Trp Glu Ala Asn
 145 150 155 160
 Trp Pro Gln His Leu Ala Gly Ala Tyr Val Ser Ser Gly Met Val Asn
 165 170 175
 Gln Ala Ala Asp Phe Val Ala Gly Lys Leu Gln
 180 185

(2) INFORMATION FOR SEQ ID NO: 15:

138

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1198 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Mycobacterium tuberculosis
 (B) STRAIN: H37Rv
- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 261..998
- (ix) FEATURE:
 (A) NAME/KEY: mat_peptide
 (B) LOCATION: 261..998

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

CAGATGCTGC GCRACATGTT TCTCGGCGAT CCGGCAGCCA ACACCGATCG AGTGCTTGAC	60
TTTTCACCG CCGTACACCG CCGACTGTTT TTCTCACCCA CCATCGACTT TCTCGACCAT	120
CCACCGCCCC TACCGCAGCG GCGCAGCCCA ACTCTGGCAG CCGGGTGGCT ATCGATCGGC	180
AGCTTGAAAG GAAGCCCCCG ATG AAC AAT CTC TAC CGC GAT TTG GCA CGG	230
Met Asn Asn Leu Tyr Arg Asp Leu Ala Pro	
1 5 10	
GTC ACC GAA GCC GCT TGG GCG GAA ATC GAA TTG GAG GCG GCG CGG ACG	278
Val Thr Glu Ala Ala Trp Ala Glu Ile Glu Leu Glu Ala Ala Arg Thr	
15 20 25	
TTC AAG CGA CAC ATC GCC GGG CAC CGG GTG GTC GAT GTC AGT GAT CCC	326
Phe Lys Arg His Ile Ala Gly Arg Arg Val Val Asp Val Ser Asp Pro	
30 35 40	
GGG GGG CCC GTC ACC GCG GCG GTC AGC ACC GGC CGG CTG ATC GAT GTT	374
Gly Gly Pro Val Thr Ala Ala Val Ser Thr Gly Arg Leu Ile Asp Val	
45 50 55	
AAG GCA CCA ACC AAC GCG GTG ATC GCC CAC CTG CGG GCC AGC AAA CCC	422
Lys Ala Pro Thr Asn Gly Val Ile Ala His Leu Arg Ala Ser Lys Pro	
60 65 70	
CTT GTC CGG CTA CAG GTT CCG TTT ACC CTG TCG CCG AAC GAG ATC GAC	470
Leu Val Arg Leu Arg Val Pro Phe Thr Leu Ser Arg Asn Glu Ile Asp	
75 80 85 90	
GAC GTG GAA CGT GGC TCT AAG GAC TCC GAT TGG GAA CGG GTA AAG GAG	518
Asp Val Glu Arg Gly Ser Lys Asp Ser Asp Trp Glu Pro Val Lys Glu	
95 100 105	

139

GCG GCC AAG AAG CTG GCC TTC GTC GAG GAC CGC ACA ATA TTC GAA GGC Ala Ala Lys Lys Leu Ala Phe Val Glu Asp Arg Thr Ile Phe Glu Gly 110 115 120	566
TAC AGC GCC GCA TCA ATC GAA GGG ATC CGC AGC GCG AGT TCG AAC CCG Tyr Ser Ala Ala Ser Ile Glu Gly Ile Arg Ser Ala Ser Ser Asn Pro 125 130 135	614
GCG CTG ACG TTG CCC GAG GAT CCC CGT GAA ATC CCT GAT GTC ATC TCC Ala Leu Thr Leu Pro Glu Asp Pro Arg Glu Ile Pro Asp Val Ile Ser 140 145 150	662
CAG GCA TTG TCC GAA CTG CGG TTG GCC GGT GTG GAC GGA CCG TAT TCG Gln Ala Leu Ser Ala Leu Arg Leu Ala Gly Val Asp Gly Pro Tyr Ser Asp 155 160 165 170	710
GTG TTG CTC TCT GCT GAC GTC TAC ACC AAG GTT AGC GAG ACT TCC GAT Val Leu Leu Ser Ala Asp Val Tyr Thr Lys Val Ser Glu Thr Ser Asp 175 180 185	758
CAC GGC TAT CCG ATC CGT GAG CAT CTG AAC CGG CTG GTG GAC GGG GAC His Gly Tyr Pro Ile Arg Glu His Leu Asn Arg Leu Val Asp Gly Asp 190 195 200	806
ATC ATT TGG GCC CCG GCC ATC GAC GCG GCG TTC GTG CTG ACC ACT CGA Ile Ile Trp Ala Pro Ala Ile Asp Gly Ala Phe Val Leu Thr Thr Arg 205 210 215	854
GGC GGC GAC TTC GAC CTA CAG CTG GGC ACC GAC GTT GCA ATC GGG TAC Gly Gly Asp Phe Asp Leu Gln Leu Gly Thr Asp Val Ala Ile Gly Tyr 220 225 230	902
GCC AGC CAC GAC ACG GAC ACC GAG CGC CTC TAC CTG CAG GAG ACG CTG Ala Ser His Asp Thr Asp Thr Glu Arg Leu Tyr Leu Gln Glu Thr Leu 235 240 245 250	950
ACG TTC CTT TGC TAC ACC GCC GAG GCG TCG GTC GCG CTC AGC CAC TAA Thr Phe Leu Cys Tyr Thr Ala Glu Ala Ser Val Ala Leu Ser His 255 260 265	998
GGCAGGAGCG CGAGCAATAG CTCCTATGGC AAGCGGCCGC GGCTTGGGTG TGTTCCGAGC	1058
TGGGCTGGTG GACGGTGCCG AGGGCCTGGA AGACGGTGCG GGCTAGGCGG CTTTGGAGCC	1118
AGCCTAGTGC TGCGCGTTTG GTTTTCCCGG CTTCTGCGAG CTTTGGGTAG TAGGCTGTGC	1178
CCCGGCTGTC GGTCAATCCGG	1198

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

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Met Asn Asn Leu Tyr Arg Asp Leu Ala Pro Val Thr Glu Ala Ala Trp
 1           5           10           15
Ala Glu Ile Glu Leu Glu Ala Ala Arg Thr Phe Lys Arg His Ile Ala
           20           25           30
Gly Arg Arg Val Val Asp Val Ser Asp Pro Gly Gly Pro Val Thr Ala
           35           40           45
Ala Val Ser Thr Gly Arg Leu Ile Asp Val Lys Ala Pro Thr Asn Gly
           50           55           60
Val Ile Ala His Leu Arg Ala Ser Lys Pro Leu Val Arg Leu Arg Val
           65           70           75           80
Pro Phe Thr Leu Ser Arg Asn Glu Ile Asp Asp Val Glu Arg Gly Ser
           85           90           95
Lys Asp Ser Asp Trp Glu Pro Val Lys Glu Ala Ala Lys Lys Leu Ala
           100          105          110
Phe Val Glu Asp Arg Thr Ile Phe Glu Gly Tyr Ser Ala Ala Ser Ile
           115          120          125
Glu Gly Ile Arg Ser Ala Ser Ser Asn Pro Ala Leu Thr Leu Pro Glu
           130          135          140
Asp Pro Arg Glu Ile Pro Asp Val Ile Ser Gln Ala Leu Ser Glu Leu
           145          150          155          160
Arg Leu Ala Gly Val Asp Gly Pro Tyr Ser Val Leu Leu Ser Ala Asp
           165          170          175
Val Tyr Thr Lys Val Ser Glu Thr Ser Asp His Gly Tyr Pro Ile Arg
           180          185          190
Glu His Leu Asn Arg Leu Val Asp Gly Asp Ile Ile Trp Ala Pro Ala
           195          200          205
Ile Asp Gly Ala Phe Val Leu Thr Thr Arg Gly Gly Asp Phe Asp Leu
           210          215          220
Gln Leu Gly Thr Asp Val Ala Ile Gly Tyr Ala Ser His Asp Thr Asp
           225          230          235          240
Thr Glu Arg Leu Tyr Leu Gln Glu Thr Leu Thr Phe Leu Cys Tyr Thr
           245          250          255
Ala Glu Ala Ser Val Ala Leu Ser His
           260          265

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(2) INFORMATION FOR SEQ ID NO: 17:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

141

(i) MOLECULE TYPE: peptide
(v) FRAGMENT TYPE: N-terminal
(vi) ORIGINAL SOURCE:
(A) ORGANISM: Mycobacterium tuberculosis
(B) STRAIN: H37Rv

(ix) FEATURE:
(A) NAME/KEY: Duplication
(B) LOCATION: 1
(D) OTHER INFORMATION: Ala is Ala or Ser

(ix) FEATURE:
(A) NAME/KEY: Duplication
(B) LOCATION: 13
(D) OTHER INFORMATION: Xaa is unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

Ala	Glu	Leu	Asp	Ala	Pro	Ala	Gly	Ala	Gly	Thr	Glu	Xaa	Ala	Val
1				5					10					15

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide
(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Mycobacterium tuberculosis
(B) STRAIN: H37Rv

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

Ala	Gln	Ile	Thr	Leu	Arg	Gly	Asn	Ala	Ile	Asn	Thr	Val	Gly	Glu
1				5					10					15

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

142

- (v) FRAGMENT TYPE: N-terminal
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Mycobacterium tuberculosis*
(B) STRAIN: H37Rv
- (ix) Feature:
(A) NAME/KEY: Other
(B) LOCATION: 3
(C) OTHER INFORMATION: Xaa is unknown
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:
- | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Pro | Xaa | Ser | Asp | Ile | Ala | Val | Val | Phe | Ala | Arg | Gly | Thr | His |
| 1 | | | 5 | | | | | 10 | | | | | 15 | |
- (2) INFORMATION FOR SEQ ID NO: 20:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (v) FRAGMENT TYPE: N-terminal
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Mycobacterium tuberculosis*
(B) STRAIN: H37Rv
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:
- | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Asp | Ser | Pro | Ileu | Ala | Thr | Ala | Thr | Ala | Thr | Leu | His | Thr | Asp |
| 1 | | | 5 | | | | | 10 | | | | | 15 | |
- (2) INFORMATION FOR SEQ ID NO: 21:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (v) FRAGMENT TYPE: N-terminal
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Mycobacterium tuberculosis*
(B) STRAIN: H37Rv
- (ix) Feature:
(A) NAME/KEY: Other
(B) LOCATION: 3

143

(C) OTHER INFORMATION: Xaa is unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

Ala	Xaa	Pro	Asp	Ala	Glu	Val	Val	Phe	Ala	Arg	Gly	Arg	Phe	Glu
1				5				10					15	

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mycobacterium tuberculosis
- (B) STRAIN: H37Rv

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1
- (C) OTHER INFORMATION: Xaa is unknown

(ix) FEATURE:

- (A) NAME/KEY: Duplication
- (B) LOCATION: 2
- (D) OTHER INFORMATION: Ile is Ile or Val

(ix) FEATURE:

- (A) NAME/KEY: Duplication
- (B) LOCATION: 10
- (D) OTHER INFORMATION: Val is Val or Thr

(ix) FEATURE:

- (A) NAME/KEY: Duplication
- (B) LOCATION: 11
- (D) OTHER INFORMATION: Val is Val or Phe

(ix) FEATURE:

- (A) NAME/KEY: Duplication
- (B) LOCATION: 14
- (D) OTHER INFORMATION: Asp is Asp or Gln

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

Xaa	Ile	Gln	Lys	Ser	Leu	Glu	Leu	Ile	Val	Val	Thr	Ala	Asp	Glu
1					5				10				15	

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:

144

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mycobacterium tuberculosis
- (B) STRAIN: H37Rv

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

Met	Asn	Asn	Leu	Tyr	Arg	Asp	Leu	Ala	Pro	Val	Thr	Glu	Ala	Ala	Trp
1			5						10					15	

Ala Glu Ile

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

CCCGGCTCGA GAACCTTAC CGGACCTSG CACC

34

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

GGGCGGATC CGAGCGGCG TCCTTACSG GTTGCCA

37

(2) INFORMATION FOR SEQ ID NO: 26:

145

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

GGAGGCCCA TATGAACAT CTCTACG

28

(2) INFORMATION FOR SEQ ID NO: 27:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

CGCGCTCAG CCTTAGTGAC TGAGCGGAC CG

32

(2) INFORMATION FOR SEQ ID NO: 28:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (synthetic)
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

CTCGAATTC CCGGTGCAC ACAG

24

(2) INFORMATION FOR SEQ ID NO: 29:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

146

(ii) MOLECULE TYPE: DNA (synthetic)

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

CTCGAATTTCG CCCCCATACG AGAAC

25

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

GTGTATCTGC TGGAC

15

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

CCGACTGGCT GCGCG

15

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

147

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

GAGGAATTCG CTTAGCGGAT CGCA

26

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

CCACATTCG GTTGG

15

(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

GTCCAGCGCA TACAC

15

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(iv) ANTI-SENSE: NO

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:
GTACGAGAAT TCATGTGCGA AATCATG 27
- (2) INFORMATION FOR SEQ ID NO: 36:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (synthetic)
 - (iv) ANTI-SENSE: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:
GTACGAGAAT TCGAGCTTGG GGTGCCG 27
- (2) INFORMATION FOR SEQ ID NO: 37:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (synthetic)
 - (iv) ANTI-SENSE: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:
CGATTCCCAAG CTGTGTGCCG CCGACCCG 28
- (2) INFORMATION FOR SEQ ID NO: 38:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (synthetic)
 - (iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

CGTTAGGGAT CCTCATGCC ATGGTGTGG

30

(2) INFORMATION FOR SEQ ID NO: 39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

CGTTAGGGAT CCGGTTCCAC TGTGCC

26

(2) INFORMATION FOR SEQ ID NO: 40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

CGTTAGGGAT CCTCAGGTCT TTTCGATG

28

(2) INFORMATION FOR SEQ ID NO: 41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 952 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mycobacterium tuberculosis
- (B) STRAIN: H37Rv

150

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 45..944

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 45..143

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
(B) LOCATION: 144..941

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

GAATTGCGCG GGTGCACACA GCCTTACACG ACGGAGGTGG ACAC ATG AAG GGT CGG	96
Met Lys Gly Arg	
-33 -30	
TCG GCG CTG CTG CCG GCG CTC TGG ATT GCC GCA CTG TCA TTC GGG TTG	104
Ser Ala Leu Leu Arg Ala Leu Trp Ile Ala Ala Leu Ser Phe Gly Leu	
-25 -20 -15	
GGC GGT GTC GCG GTA GCC GCG GAA CCC ACC GCC AAG GCC GGC CCA TAC	152
Gly Gly Val Ala Val Ala Ala Glu Pro Thr Ala Lys Ala Ala Pro Tyr	
-10 -5 1	
GAG AAC CTG ATG GTG CCG TCG CCC TCG ATG GGC CGG GAC ATC CCG GTG	200
Glu Asn Leu Met Val Pro Ser Pro Ser Met Gly Arg Asp Ile Pro Val	
5 10 15	
GCC TTC CTA GCC GGT GGG CCG CAC GCG GTG TAT CTG CTG GAC GCC TTC	248
Ala Phe Leu Ala Gly Gly Pro His Ala Val Tyr Leu Leu Asp Ala Phe	
20 25 30 35	
AAC GCC GGC CCG GAT GTC AGT AAC TGG GTC ACC GCG GGT AAC GCG ATG	296
Asp Ala Gly Pro Asp Val Ser Asn Trp Val Thr Ala Gly Asn Ala Met	
40 45 50	
AAC ACG TTG GCG GGC AAG GGG ATT TCG GTG GTG GCA CCG GCC GGT GGT	344
Asn Thr Leu Ala Gly Lys Gly Ile Ser Val Val Ala Pro Ala Gly Gly	
55 60 65	
GCG TAC AGC ATG TAC ACC AAC TGG GAG CAG GAT GCC AGC AAG CAG TGG	392
Ala Tyr Ser Met Tyr Thr Asn Trp Glu Glu Asp Gly Ser Lys Glu Trp	
70 75 80	
GAC ACC TTC TTG TCC GCT GAG CTG CCC GAC TGG CTG GCG GCT AAC CCG	440
Asp Thr Phe Leu Ser Ala Glu Leu Pro Asp Trp Leu Ala Ala Asn Arg	
85 90 95	
GGC TTG GCC CCC GGT GGC CAT GCG GCC GTT GCG GCC GCT CAG GCG GGT	488
Gly Leu Ala Pro Gly Gly His Ala Ala Val Gly Ala Ala Gln Gly Gly	
100 105 110 115	
TAC GGG GCG ATG GCG CTG GCG GCC TTC CAC CCC GAC CCG TTC GGC TTC	536
Tyr Gly Ala Met Ala Leu Ala Ala Phe His Pro Asp Arg Phe Gly Phe	
120 125 130	

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GCT GGC TCG ATG TCG GGC TTT TTG TAC CCG TCG AAC ACC ACC ACC AAC	584
Ala Gly Ser Met Ser Gly Phe Leu Tyr Pro Ser Asn Thr Thr Asn	
135 140 145	
GGT GCG ATC GCG GCG GGC ATG CAG CAA TTC GGC GGT GTG GAC ACC AAC	632
Gly Ala Ile Ala Ala Gly Met Gln Gln Phe Gly Gly Val Asp Thr Asn	
150 155 160	
GGG ATG TGG GGA GCA CCA CAG CTG GGT CCG TGG AAG TGG CAC GAC CCG	680
Gly Met Trp Gly Ala Pro Gln Leu Gly Arg Trp Lys Trp His Asp Pro	
165 170 175	
TGG GTG CAT GCC AGC CTG CTG GCG CAA AAC AAC ACC CCG GTG TGG GTG	728
Trp Val His Ala Ser Leu Leu Ala Gln Asn Asn Thr Arg Val Trp Val	
180 185 190 195	
TGG AGC CCG ACC AAC CCG GGA GCC AGC GAT CCC GCC GCC ATG ATC GGC	776
Trp Ser Pro Thr Asn Pro Gly Ala Ser Asp Pro Ala Ala Met Ile Gly	
200 205 210	
CAA ACC GCC GAG GCG ATG GGT AAC AGC CGC ATG TTC TAC AAC CAG TAT	824
Gln Thr Ala Glu Ala Met Gly Asn Ser Arg Met Phe Tyr Asn Gln Tyr	
215 220 225	
CGC AGC GTC GGC GGG CAC AAC GGA CAC TTC GAC TTC CCA GCC AGC GGT	872
Arg Ser Val Gly Gly His Asn Gly His Phe Asp Phe Pro Ala Ser Gly	
230 235 240	
GAC AAC GGC TGG GGC TCG TGG GCG CCC CAG CTG GGC GCT ATG TGG GGC	920
Asp Asn Gly Trp Gly Ser Trp Ala Pro Gln Leu Gly Ala Met Ser Gly	
245 250 255	
GAT ATC GTC GGT GCG ATC CGC TAA GCGAATTC	952
Asp Ile Val Gly Ala Ile Arg	
260 265	

(2) INFORMATION FOR SEQ ID NO: 42:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 299 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

Met Lys Gly Arg Ser Ala Leu Leu Arg Ala Leu Trp Ile Ala Ala Leu	
-33 -30 -25 -20	
Ser Phe Gly Leu Gly Gly Val Ala Val Ala Ala Glu Pro Thr Ala Lys	
-15 -10 -5	
Ala Ala Pro Tyr Glu Asn Leu Met Val Pro Ser Pro Ser Met Gly Arg	
1 5 10 15	
Asp Ile Pro Val Ala Phe Leu Ala Gly Gly Pro His Ala Val Tyr Leu	
20 25 30	

152

Leu	Asp	Ala	Phe	Asn	Ala	Gly	Pro	Asp	Val	Ser	Asn	Trp	Val	Thr	Ala
			35					40							45
Gly	Asn	Ala	Met	Asn	Thr	Leu	Ala	Gly	Lys	Gly	Ile	Ser	Val	Val	Ala
		50					55					60			
Pro	Ala	Gly	Gly	Ala	Tyr	Ser	Met	Tyr	Thr	Asn	Trp	Glu	Gln	Asp	Gly
		65				70					75				
Ser	Lys	Gln	Trp	Asp	Thr	Phe	Leu	Ser	Ala	Glu	Leu	Pro	Asp	Trp	Leu
		80			85					90				95	
Ala	Ala	Asn	Arg	Gly	Leu	Ala	Pro	Gly	Gly	His	Ala	Ala	Val	Gly	Ala
			100					105						110	
Ala	Gln	Gly	Gly	Tyr	Gly	Ala	Met	Ala	Leu	Ala	Ala	Phe	His	Pro	Asp
		115					120						125		
Arg	Phe	Gly	Phe	Ala	Gly	Ser	Met	Ser	Gly	Phe	Leu	Tyr	Pro	Ser	Asn
		130					135					140			
Thr	Thr	Thr	Asn	Gly	Ala	Ile	Ala	Ala	Gly	Met	Gln	Gln	Phe	Gly	Gly
		145				150					155				
Val	Asp	Thr	Asn	Gly	Met	Trp	Gly	Ala	Pro	Gln	Leu	Gly	Arg	Trp	Lys
		160			165					170				175	
Trp	His	Asp	Pro	Trp	Val	His	Ala	Ser	Leu	Leu	Ala	Gln	Asn	Asn	Thr
			180					185						190	
Arg	Val	Trp	Val	Trp	Ser	Pro	Thr	Asn	Pro	Gly	Ala	Ser	Asp	Pro	Ala
		195						200					205		
Ala	Met	Ile	Gly	Gln	Thr	Ala	Glu	Ala	Met	Gly	Asn	Ser	Arg	Met	Phe
		210					215						220		
Tyr	Asn	Gln	Tyr	Arg	Ser	Val	Gly	Gly	His	Asn	Gly	His	Phe	Asp	Phe
		225				230				235					
Pro	Ala	Ser	Gly	Asp	Asn	Gly	Trp	Gly	Ser	Trp	Ala	Pro	Gln	Leu	Gly
		240			245					250				255	
Ala	Met	Ser	Gly	Asp	Ile	Val	Gly	Ala	Ile	Arg					
			260					265							

(2) INFORMATION FOR SEQ ID NO: 43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

GCAACACCCG GGATGTGCGA AATCATG

27

(2) INFORMATION FOR SEQ ID NO: 44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

GTAACACCCG GGGTGGCCGC CGACCCG

27

(2) INFORMATION FOR SEQ ID NO: 45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

CTACTAGGCT TGGATCCCTA GCGGCCCAT TTGGCGG

37

(2) INFORMATION FOR SEQ ID NO: 46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(iv) ANTI-SENSE: YES

154

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

CTACTAAGCT TCCATGGTCA GGTCTTTTCG ATGCTTAC

38

(2) INFORMATION FOR SEQ ID NO: 47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 195...320

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

GTGCGCGCT CCCAGGGT CTTATGGTTC GATATACCTG AGTTGATGG AAGTCGATG	60
ACCAGCAGTC AGCATACGGC ATGGCCGAAA AGAGTGGGGT GATG ATG GCC GAG GAT	116
Met Ala Glu Asp	
1	
GTT CGC GGC GAG ATC GTG GCC AGC GTT CTG GAA GTC GTT GTC AAC GAA	164
Val Arg Ala Glu Ile Val Ala Ser Val Leu Glu Val Val Val Asn Glu	
5 10 15 20	
GGC GAT CAG ATC GAC AAG GGC GAC GTC GTG GTG CTG CTG GAG TCG ATG	212
Gly Asp Gln Ile Asp Lys Gly Asp Val Val Val Leu Leu Glu Ser Met	
25 30 35	
AAG ATG GAG ATC CCC GTC CTG GCC GAA GCT GCC GGA ACG GTC AGC AAG	260
Lys Met Glu Ile Pro Val Leu Ala Glu Ala Ala Gly Thr Val Ser Lys	
40 45 50	
GTG GCG GTA TCG GTG GGC GAT GTC ATT CAG GCC GGC GAC CTT ATC GCG	308
Val Ala Val Ser Val Gly Asp Val Ile Gln Ala Gly Asp Leu Ile Ala	
55 60 65	
GTG ATC AGC TAGTCGTTGA TAGTCACTCA TGTCCACACT CGGTGATCTG CTCGCGAA	366
Val Ile Ser	
70	
CACACGGTGC TGCAGGAC CAGCGTGGAC CAGCTGCATG CAGTGTCTGG GAGTGGCAG	426
CTCTTGCCG ACTGTCTT TGCC	450

(2) INFORMATION FOR SEQ ID NO: 48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

155

(D) TOPOLOGY: linear

(iii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

```

Met Ala Glu Asp Val Arg Ala Glu Ile Val Ala Ser Val Leu Glu Val
 1             S             10             15
Val Val Asn Glu Gly Asp Gln Ile Asp Lys Gly Asp Val Val Val Leu
          20             25             30
Leu Glu Ser Met Lys Met Glu Ile Pro Val Leu Ala Glu Ala Ala Gly
          35             40             45
Thr Val Ser Lys Val Ala Val Ser Val Gly Asp Val Ile Gln Ala Gly
          50             55             60
Asp Leu Ile Ala Val Ile Ser
65             70

```

(2) INFORMATION FOR SEQ ID NO: 49:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 750 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 113...640

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

```

GGGTACCCCT CGATGGGTTG CGGTTGGCA CCGAGGTGCT AACGCACCTG CTGACACACT      60
GCTAGTGGAA AACGAGGCTA GTGCAACGT CGATCACAGC AGAGGACTGA CC ATG ACA      118
                                     Met Thr
                                     1
ACT TCA CCC GAC CCG TAT GCC GCG CTG CCC AAG CTG CCG TCC TTC AGC      166
Thr Ser Pro Asp Pro Tyr Ala Ala Leu Pro Lys Leu Pro Ser Phe Ser
          5             10             15
CTG ACG TCA ACC TCG ATC ACC GAT GGG CAG CCG CTG GCT ACA CCC CAG      214
Leu Thr Ser Thr Ser Ile Thr Asp Gly Gln Pro Leu Ala Thr Pro Gln
          20             25             30
GTC AGC GGG ATC ATG GGT CCG GGC GGG GCG GAT GCC AGT CCG CAG CTG      262
Val Ser Gly Ile Met Gly Ala Gly Gly Ala Asp Ala Ser Pro Gln Leu
          35             40             45             50

```

156

AGG TGG TCG GGA TTT CCC AGC GAG ACC CGC AGC TTC GCG GTA ACC GTC	310
Arg Trp Ser Gly Phe Pro Ser Glu Thr Arg Ser Phe Ala Val Thr Val	
55 60 55	
TAC GAC CCT GAT GCC CCC ACC CTG TCC GGG TTC TGG CAC TGG GCG GTG	358
Tyr Asp Pro Asp Ala Pro Thr Leu Ser Gly Phe Trp His Trp Ala Val	
70 75 80	
GCC AAC CTG CCT GGC AAC GTC ACC GAG TTG CCC GAG GGT GTC GGC GAT	406
Ala Asn Leu Pro Ala Asn Val Thr Glu Leu Pro Glu Gly Val Gly Asp	
85 90 95	
GGC CGC GAA CTG CCG GGC GGG GCA CTG ACA TTG GTC AAC GAC GCC GGT	454
Gly Arg Glu Leu Pro Gly Gly Ala Leu Thr Leu Val Asn Asp Ala Gly	
100 105 110	
ATG CGC CGG TAT GTG GGT GCG GCG CCG CCT CCC GGT CAT GGG GTG CAT	502
Met Arg Arg Tyr Val Gly Ala Ala Pro Pro Gly His Gly Val His	
115 120 125 130	
CGC TAC TAC GTC GCG GTA CAC GCG GTG AAG GTC GAA AAG CTC GAC CTC	550
Arg Tyr Tyr Val Ala Val His Ala Val Lys Val Glu Lys Leu Asp Leu	
135 140 145	
CCC GAG GAC GCG AGT CCT GCA TAT CTG GGA TTC AAC CTG TTC CAG CAC	598
Pro Glu Asp Ala Ser Pro Ala Tyr Leu Gly Phe Asn Leu Phe Glu His	
150 155 160	
GCG APT GCA CGA GCG GTC ATC TTC GGC ACC TAC GAG CAG CGT TAGCGCTTT	649
Ala Ile Ala Arg Ala Val Ile Phe Gly Thr Tyr Glu Glu Arg	
165 170 175	
AGCTGGGTTG CCGAGCTTT GCGGAGCGGA CCGCTCCTG CAGGAGCCG AACCGCGGT	709
CAAGCAGCCT GCGGGCAATG CTTTCATGGA TGTCCTTGGC C	750

(2) INFORMATION FOR SEQ ID NO: 50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 176 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iv) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

Met Thr Thr Ser Pro Asp Pro Tyr Ala Ala Leu Pro Lys Leu Pro Ser	
1 5 10 15	
Phe Ser Leu Thr Ser Thr Ser Ile Thr Asp Gly Glu Pro Leu Ala Thr	
20 25 30	
Pro Glu Val Ser Gly Ile Met Gly Ala Gly Gly Ala Asp Ala Ser Pro	
35 40 45	

157

Gln	Leu	Arg	Trp	Ser	Gly	Phe	Pro	Ser	Glu	Thr	Arg	Ser	Phe	Ala	Val	
50							55					60				
Thr	Val	Tyr	Asp	Pro	Asp	Ala	Pro	Thr	Leu	Ser	Gly	Phe	Trp	His	Trp	
65					70					75					80	
Ala	Val	Ala	Asn	Leu	Pro	Ala	Asn	Val	Thr	Glu	Leu	Pro	Glu	Gly	Val	
					85					90					95	
Gly	Asp	Gly	Arg	Glu	Leu	Pro	Gly	Gly	Ala	Leu	Thr	Leu	Val	Asn	Asp	
					100				105					110		
Ala	Gly	Met	Arg	Arg	Tyr	Val	Gly	Ala	Ala	Pro	Pro	Pro	Gly	His	Gly	
					115				120					125		
Val	His	Arg	Tyr	Tyr	Val	Ala	Val	His	Ala	Val	Lys	Val	Glu	Lys	Leu	
					130				135					140		
Asp	Leu	Pro	Glu	Asp	Ala	Ser	Pro	Ala	Tyr	Leu	Gly	Phe	Asn	Leu	Phe	
145					150					155					160	
Gln	His	Ala	Ile	Ala	Arg	Ala	Val	Ile	Phe	Gly	Thr	Tyr	Glu	Gln	Arg	
					165				170						175	

(2) INFORMATION FOR SEQ ID NO: 51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 888 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 18...685
- (D) OTHER INFORMATION:

- (A) NAME/KEY: Signal Sequence
- (B) LOCATION: 18...134
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

TCATGAGGTT CATCGGG GTG ATC CCA GCG CCG CAG CGC CAT TCG GAG CGC	50		
Met Ile Pro Arg Pro Gln Pro His Ser Gly Arg			
-35	-30		
TGG CGA GCC GGT GCC GCA CGC CGC CTC ACC AGC CTG GTG GCC GCC GCC	95		
Trp Arg Ala Gly Ala Ala Arg Arg Leu Thr Ser Leu Val Ala Ala Ala			
-25	-20	-15	
TTT GCG GCG GCC ACA CTG TTG CTT ACC CCC GCG CTG GCA CCA CCG GCA	146		
Phe Ala Ala Ala Thr Leu Leu Leu Thr Pro Ala Leu Ala Pro Pro Ala			
-10	-5	1	5

158

TCG GCG GGC TGC CCG GAT GCC GAG GTG GTG TTC GCC CGC GGA ACC GGC	194
Ser Ala Gly Cys Pro Asp Ala Glu Val Val Phe Ala Arg Gly Thr Gly	
10 15 20	
GAA CCA CCT GGC CTC GGT CGG GTA GGC CAA GCT TTC GTC AGT TCA TTG	242
Glu Pro Pro Gly Leu Gly Arg Val Gly Gln Ala Phe Val Ser Ser Leu	
25 30 35	
CGC CAG CAG ACC AAC AAG AGC ATC GCG ACA TAC GGA GTC AAC TAC CCG	290
Arg Gln Gln Thr Asn Lys Ser Ile Gly Thr Tyr Gly Val Asn Tyr Pro	
40 45 50	
GCC AAC GGT GAT TTC TTG GCC GCC GCT GAC GGC GCG AAC GAC GCC AGC	338
Ala Asn Gly Asp Phe Leu Ala Ala Ala Asp Gly Ala Asn Asp Ala Ser	
55 60 65	
GAC CAC ATT CAG CAG ATG GCC AGC GCG TGC CGG GCC ACG AGG TTG GTG	386
Asp His Ile Gln Gln Met Ala Ser Ala Cys Arg Ala Thr Arg Leu Val	
70 75 80 85	
CTC GGC GGC TAC TCC CAG GGT GCG GCC GTG ATC GAC ATC GTC ACC GCC	434
Leu Gly Gly Tyr Ser Gln Gly Ala Ala Val Ile Asp Ile Val Thr Ala	
90 95 100	
GCA CCA CTG CCC GGC CTC GGG TTC ACG CAG CCG TTG CCG CCC GCA GCG	482
Ala Pro Leu Pro Gly Leu Gly Phe Thr Gln Pro Leu Pro Pro Ala Ala	
105 110 115	
GAC GAT CAC ATC GCC GCG ATC GCG CTG TTC GGG AAT CCC TCG GGC CGC	530
Asp Asp His Ile Ala Ala Ile Ala Leu Phe Gly Asn Pro Ser Gly Arg	
120 125 130	
GCT GGC GGC CTG ATG AGC GCC CTG ACC CCT CAA TTC GGG TCC AAG ACC	578
Ala Gly Gly Leu Met Ser Ala Leu Thr Pro Gln Phe Gly Ser Lys Thr	
135 140 145	
ATC AAC CTC TGC AAC AAC GGC GAC CCG ATT TGT TCG GAC GGC AAC CGG	626
Ile Asn Leu Cys Asn Asn Gly Asp Pro Ile Cys Ser Asp Gly Asn Arg	
150 155 160 165	
TGG CGA GCG CAC CTA GGC TAC GTG CCC GGG ATG ACC AAC CAG GCG GCG	674
Trp Arg Ala His Leu Gly Tyr Val Pro Gly Met Thr Asn Gln Ala Ala	
170 175 180	
GCT TTC GTC GCG AGC AGG ATC TAAACCGAGC CGCCCCATAG ATTCCGGGCTA AGCA	722
Arg Phe Val Ala Ser Arg Ile	
185	
ACGGCTGGCG CGCGCGCCGG CCACGAGTGA CGCGCGCGGA CTGGCACACC GCTTACCAAG	789
GCCTATGCT G	836

(2) INFORMATION FOR SEQ ID NO: 52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 226 amino acids
 (B) TYPE: amino acid

159

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal
(ix) FEATURE:

(A) NAME/KEY: Signal Sequence
(B) LOCATION: 1...38
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

```

Met Ile Pro Arg Pro Gln Pro His Ser Gly Arg Trp Arg Ala Gly Ala
   -35                               -30                               -25

Ala Arg Arg Leu Thr Ser Leu Val Ala Ala Ala Phe Ala Ala Ala Thr
   -20                               -15                               -10

Leu Leu Leu Thr Pro Ala Leu Ala Pro Pro Ala Ser Ala Gly Cys Pro
   -5                               1                               5                               10

Asp Ala Glu Val Val Phe Ala Arg Gly Thr Gly Glu Pro Pro Gly Leu
   15                               20                               25

Gly Arg Val Gly Gln Ala Phe Val Ser Ser Leu Arg Gln Gln Thr Asn
   30                               35                               40

Lys Ser Ile Gly Thr Tyr Gly Val Asn Tyr Pro Ala Asn Gly Asp Phe
   45                               50                               55

Leu Ala Ala Ala Asp Gly Ala Asn Asp Ala Ser Asp His Ile Gln Gln
   60                               65                               70

Met Ala Ser Ala Cys Arg Ala Thr Arg Leu Val Leu Gly Gly Tyr Ser
   75                               80                               85                               90

Gln Gly Ala Ala Val Ile Asp Ile Val Thr Ala Ala Pro Leu Pro Gly
   95                               100                               105

Leu Gly Phe Thr Gln Pro Leu Pro Pro Ala Ala Asp Asp His Ile Ala
  110                               115                               120

Ala Ile Ala Leu Phe Gly Asn Pro Ser Gly Arg Ala Gly Gly Leu Met
  125                               130                               135

Ser Ala Leu Thr Pro Gln Phe Gly Ser Lys Thr Ile Asn Leu Cys Asn
  140                               145                               150

Asn Gly Asp Pro Ile Cys Ser Asp Gly Asn Arg Trp Arg Ala His Leu
  155                               160                               165                               170

Gly Tyr Val Pro Gly Met Thr Asn Gln Ala Ala Arg Phe Val Ala Ser
  175                               180                               185

Arg Ile

```

(2) INFORMATION FOR SEQ ID NO: 53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 700 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 73...615
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

CTAGGAAGGC	CYTTCCTGAG	TAAGTATGCG	CTTCGTTGCA	TACCGCCCTT	TACCTGGCTT	60
AATCTGCATT	TT ATG ACA GAA TAC GAA GGG CCF	ARG ACA AAA TTC CAC GCG	111			
	Met Thr Glu Tyr Glu Gly Pro Lys Thr Lys Phe His Ala					
	1 5 10					
TTA ATG CAG GAA CAG ATT CMT AAC GAA TTC ACA GCG GCA CAA CAA TAT	159					
Leu Met Gln Glu Gln Ile His Asn Glu Phe Thr Ala Ala Gln Gln Tyr						
15 20 25						
GTC GCG ATC GCG GTT TAT TTC GAC AGC GAA GAC CTG CCG CAG TTG GCG	207					
Val Ala Ile Ala Val Tyr Phe Asp Ser Glu Asp Leu Pro Gln Leu Ala						
30 35 40 45						
ARG CAT TTT TAC AGC CAA GCG GTC GAG GAA CGA ARC CAT GCA ATG ATG	255					
Lys His Phe Tyr Ser Gln Ala Val Glu Glu Arg Asn His Ala Met Met						
50 55 60						
CTC GTG CAA CAC CTG CTC GAC CCG GAC CTT CGT GTC GAA ATT CCC GGC	303					
Leu Val Gln His Leu Leu Asp Arg Asp Leu Arg Val Glu Ile Pro Gly						
65 70 75						
GTA GAC ACG GTG CGA AAC CAG TTC GAC AGA CCC CCG GAG GCA CTG GCG	351					
Val Asp Thr Val Arg Asn Gln Phe Asp Arg Pro Arg Glu Ala Leu Ala						
80 85 90						
CTG GCG CTC GAT CAG GAA CCG ACA GTC ACC GAC CAG GTC GGT CGG CTG	399					
Leu Ala Leu Asp Gln Glu Arg Thr Val Thr Asp Glu Val Gly Arg Leu						
95 100 105						
ACA GCG GTG GCC CCG GAC GAG GGC GAT TTC CTC GCG GAG CAG TTC ATG	447					
Thr Ala Val Ala Arg Asp Glu Gly Asp Phe Leu Gly Glu Gln Phe Met						
110 115 120 125						
CAG TGG TTC TTG CAG GAA CAG ATC GAA GAG GTG GCC TTG ATG GCA ACC	495					
Gln Trp Phe Leu Gln Glu Gln Ile Glu Glu Val Ala Leu Met Ala Thr						
130 135 140						
CTG GTG CCG GTT GCC GAT CCG GCC GGG GCC AAC CTG TTC GAG CTA GAG	543					
Leu Val Arg Val Ala Asp Arg Ala Gly Ala Asn Leu Phe Glu Leu Glu						
145 150 155						

161

AAC TTC GTC GCA CGT GAA GTG GAT GTG GCG CCG GCC GCA TCA GGC GCC	591
Asn Phe Val Ala Arg Glu Val Asp Val Ala Pro Ala Ala Ser Gly Ala	
160 165 170	
CCG CAC GCT GCC GGG GGC CGC CTC TAGATCCCTG GCGGGGATCA GCGAGTGGTC	645
Pro His Ala Ala Gly Gly Arg Leu	
175 180	
CCGTCGCCC GCCCGTCTTC CAGCCAGGCC TTGGTGCGGC CCGGGTGGTG AGTAC	700

(2) INFORMATION FOR SEQ ID NO: 54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iv) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

Met Thr Glu Tyr	Gly Pro Lys Thr	Lys Phe His Ala	Leu Met Gln
1 5	10	15	
Glu Gln Ile His Asn Glu Phe Thr	Ala Ala Gln Gln Tyr	Val Ala Ile	
20	25	30	
Ala Val Tyr Phe Asp Ser Glu Asp Leu	Pro Gln Leu Ala	Lys His Phe	
35	40	45	
Tyr Ser Gln Ala Val Glu Glu Arg Asn His	Ala Met Met Leu	Val Gln	
50	55	60	
His Leu Leu Asp Arg Asp Leu Arg Val Glu	Ile Pro Gly Val Asp Thr		
65	70	75	80
Val Arg Asn Gln Phe Asp Arg Pro Arg Glu	Ala Leu Ala Leu Ala Leu		
85	90	95	
Asp Gln Glu Arg Thr Val Thr Asp Gln	Val Gly Arg Leu Thr Ala Val		
100	105	110	
Ala Arg Asp Glu Gly Asp Phe Leu Gly Glu Gln	Phe Met Gln Trp Phe		
115	120	125	
Leu Gln Glu Gln Ile Glu Glu Val Ala Leu	Met Ala Thr Leu Val Arg		
130	135	140	
Val Ala Asp Arg Ala Gly Ala Asn Leu Phe	Glu Leu Glu Asn Phe Val		
145	150	155	160
Ala Arg Glu Val Asp Val Ala Pro Ala	Ala Ser Gly Ala Pro His Ala		
165	170	175	

162

Ala Gly Gly Arg Leu
180

(2) INFORMATION FOR SEQ ID NO: 55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 950 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
(B) LOCATION: 133...918
(D) OTHER INFORMATION:

- (A) NAME/KEY: Signal Sequence
(B) LOCATION: 133...233
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

TGGGCTGGGC ACTGGCTCTC CCACGGTGGC GCGCTGATT CTCGCCACGG TAGGGGTTGC	60
GAGGCATOTT CTTCACGGTC TATCCACAGC TACCGACATT TGCTTCGGCT GGATCGGGG	120
TAAATTCGG TC GTG AAC AAT CGA CCC ATC CGC CTG CTG ACA TCC GGC AGG	171
Met Asn Asn Arg Pro Ile Arg Leu Leu Thr Ser Gly Arg	
-30 -25	
GCT GGT TTG GGT GCG GGC GCA TTG ATC ACC GCC CTC GTC CTG CTC ATC	219
Ala Gly Leu Gly Ala Gly Ala Leu Ile Thr Ala Val Val Leu Leu Ile	
-20 -15 -10 -5	
GCC TTG GGC GCT GTT TGG ACC CCG GTT GCC TTC GCC GAT GGA TGC CCG	267
Ala Leu Gly Ala Val Trp Thr Pro Val Ala Phe Ala Asp Gly Cys Pro	
1 5 10	
GAC GCC GAA CTC ACG TTC GCC CGC GGC ACC GGC GAG CCG CCC GGA ATC	315
Asp Ala Glu Val Thr Phe Ala Arg Gly Thr Gly Glu Pro Pro Gly Ile	
15 20 25	
GGG CGC GTT GGC CAG GCG TTC GTC GAC TCG CTG CGC CAG CAG ACT GGC	363
Gly Arg Val Gly Gln Ala Phe Val Asp Ser Leu Arg Gln Gln Thr Gly	
30 35 40	
ATG GAG ATC GGA GTA TAC CCG GTG AAT TAC GCC GCC AGC CGC CTA CAG	411
Met Glu Ile Gly Val Tyr Pro Val Asn Tyr Ala Ala Ser Arg Leu Gln	
45 50 55 60	
CTG CAC GGG GGA GAC GGC GCC AAC GAC GCC ATA TCG CAC ATT AAG TCC	459
Leu His Gly Gly Asp Gly Ala Asn Asp Ala Ile Ser His Ile Lys Ser	
65 70 75	

163

ATG GCC TCG TCA TGC CCG AAC ACC AAG CTG GTC TTG GGC GGC TAT TCG	507
Met Ala Ser Ser Cys Pro Asn Thr Lys Leu Val Leu Gly Gly Tyr Ser	
80 85 90	
CAG GGC GCA ACC GTG ATC GAT ATC GTG GCC GGG GTT CCG TTG GGC AGC	555
Gln Gly Ala Thr Val Ile Asp Ile Val Ala Gly Val Pro Leu Gly Ser	
95 100 105	
ATC AGC TTT GGC AGT CCG CTA CCT GCG GCA TAC GCA GAC AAC GTC GCA	603
Ile Ser Phe Gly Ser Pro Leu Pro Ala Ala Tyr Ala Asp Asn Val Ala	
110 115 120	
GCG GTC GCG GTC TTC GGC AAT CCG TCC AAC CCG GCC GGC GGA TCG CTG	651
Ala Val Ala Val Phe Gly Asn Pro Ser Asn Arg Ala Gly Gly Ser Leu	
125 130 135 140	
TCG AGC CTG AGC CCG CTA TTC GGT TCC AAG GCG ATT GAC CTG TGC AAT	699
Ser Ser Leu Ser Pro Leu Phe Gly Ser Lys Ala Ile Asp Leu Cys Asn	
145 150 155	
CCC ACC GAT CCG ATC TGC CAT GTG GGC CCC GGC AAC GAA TTC AGC GGA	747
Pro Thr Asp Pro Ile Cys His Val Gly Pro Gly Asn Gln Phe Ser Gly	
160 165 170	
CAC ATC GAC GGC TAC ATA CCC ACC TAC ACC ACC CAG GCG GCT AGT TTC	795
His Ile Asp Gly Tyr Ile Pro Thr Tyr Thr Thr Gln Ala Ala Ser Phe	
175 180 185	
GTC GTG CAG AGG CTC GGC GCC GGG TCG GTG CCA CAT CTG CCT GGA TCC	843
Val Val Gln Arg Leu Arg Ala Gly Ser Val Pro His Leu Pro Gly Ser	
190 195 200	
GTC CCG CAG CTG CCC GGG TCT GTC CTF CAG ATG CCC GGC ACT GCC GCA	891
Val Pro Gln Leu Pro Gly Ser Val Leu Gln Met Pro Gly Thr Ala Ala	
205 210 215 220	
CCG GCT CCC GAA TCG CTG CAC GGT GCG TGACGCTTTG TCAGTAAGCC CATAAAA	945
Pro Ala Pro Glu Ser Leu His Gly Arg	
225	
TCGCG	950

(2) INFORMATION FOR SEQ ID NO: 55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iv) FRAGMENT TYPE: internal

(ix) FEATURE:

(A) NAME/KEY: Signal Sequence

(B) LOCATION: 1...33

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

Met Asn Asn Arg Pro Ile Arg Leu Leu Thr Ser Gly Arg Ala Gly Leu
 -30 -25 -20

Gly Ala Gly Ala Leu Ile Thr Ala Val Val Leu Leu Ile Ala Leu Gly
 -15 -10 -5

Ala Val Trp Thr Pro Val Ala Phe Ala Asp Gly Cys Pro Asp Ala Glu
 1 5 10 15

Val Thr Phe Ala Arg Gly Thr Gly Glu Pro Pro Gly Ile Gly Arg Val
 20 25 30

Gly Gln Ala Phe Val Asp Ser Leu Arg Gln Gln Thr Gly Met Glu Ile
 35 40 45

Gly Val Tyr Pro Val Asn Tyr Ala Ala Ser Arg Leu Glu Leu His Gly
 50 55 60

Gly Asp Gly Ala Asn Asp Ala Ile Ser His Ile Lys Ser Met Ala Ser
 65 70 75

Ser Cys Pro Asn Thr Lys Leu Val Leu Gly Gly Tyr Ser Gln Gly Ala
 80 85 90 95

Thr Val Ile Asp Ile Val Ala Gly Val Pro Leu Gly Ser Ile Ser Phe
 100 105 110

Gly Ser Pro Leu Pro Ala Ala Tyr Ala Asp Asn Val Ala Ala Val Ala
 115 120 125

Val Phe Gly Asn Pro Ser Asn Arg Ala Gly Gly Ser Leu Ser Ser Leu
 130 135 140

Ser Pro Leu Phe Gly Ser Lys Ala Ile Asp Leu Cys Asn Pro Thr Asp
 145 150 155

Pro Ile Cys His Val Gly Pro Gly Asn Glu Phe Ser Gly His Ile Asp
 160 165 170 175

Gly Tyr Ile Pro Thr Tyr Thr Thr Gln Ala Ala Ser Phe Val Val Gln
 180 185 190

Arg Leu Arg Ala Gly Ser Val Pro His Leu Pro Gly Ser Val Pro Gln
 195 200 205

Leu Pro Gly Ser Val Leu Gln Met Pro Gly Thr Ala Ala Pro Ala Pro
 210 215 220

Glu Ser Leu His Gly Arg
 225

(2) INFORMATION FOR SEQ ID NO: 57:

165

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1069 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 94...966
 (D) OTHER INFORMATION:

- (A) NAME/KEY: Signal Sequence
 (B) LOCATION: 94...264
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

CGAGGAGACC GACGATCTGC TCGACGAAT CACGACGTC CTGAGGAGA ACGCCGAGGA	60
CTTCGTCGCG GCATACGTCC AAAAGGGCGG ACA GTG ACC TGG CCG TTG CCC GAT	114
Met Thr Trp Pro Leu Pro Asp	
-35 -50	
CGC CTG TCC ATT AAT TCA CTC TCT GGA ACA CCC GCT GTA GAC CTA TCT	162
Arg Leu Ser Ile Asn Ser Leu Ser Gly Thr Pro Ala Val Asp Leu Ser	
-45 -60 -75	
TCT TTC ACT GAC TTC CTG CGC CGC CAG GCG CCG GAG TTG CTG CCG GCA	210
Ser Phe Thr Asp Phe Leu Arg Arg Gln Ala Pro Glu Leu Leu Pro Ala	
-90 -105 -120	
AGC ATC AGC GGC GGT GCG CCA CTC GCA GGC GGC GAT GCG CAA CTG CCG	258
Ser Ile Ser Gly Gly Ala Pro Leu Ala Gly Gly Asp Ala Gln Leu Pro	
-135 -150 -165	
CAC GGC ACC ACC ATT GTC GCG CTG AAA TAC CCC GGC GGT GTT GTC ATG	306
His Gly Thr Thr Ile Val Ala Leu Lys Tyr Pro Gly Gly Val Val Met	
1 5 10 15	
GCG GGT GAC CGG COT TCG ACG CAG GGC AAC ATG ATT TCT GCG CGT GAT	354
Ala Gly Asp Arg Arg Ser Thr Gln Gly Asn Met Ile Ser Gly Arg Asp	
20 25 30	
GTG CCG AAG GTG TAT ATC ACC GAT GAC TAC ACC GCT ACC GGC ATC GCT	402
Val Arg Lys Val Tyr Ile Thr Asp Asp Tyr Thr Ala Thr Gly Ile Ala	
35 40 45	
GGC ACG GCT GCG GTC GCG GTT GAG TTT GGC CCG CTG TAT GCC GTG GAA	450
Gly Thr Ala Ala Val Ala Val Glu Phe Ala Arg Leu Tyr Ala Val Glu	
50 55 60	
CTT GAG CAC TAC GAG AAG CTC GAG GGT GTG CCG CTG ACC TTT GCC GGC	498
Leu Glu His Tyr Glu Lys Leu Glu Gly Val Pro Leu Thr Phe Ala Gly	
65 70 75	

166

AAA ATC AAC CCG CTG GCG ATT ATG GTG CGT GGC AAT CTG GCG GCC GCG	546
Lys Ile Asn Arg Leu Ala Ile Met Val Arg Gly Asn Leu Ala Ala Ala	
80 85 90 95	
ATG CAG GGT CTG CTG GCG TTG CCG TTG CTG GCG GGC TAC GAC ATT CAT	594
Met Gln Gly Leu Leu Ala Leu Pro Leu Leu Ala Gly Tyr Asp Ile His	
100 105 110	
GCG TCT GAC CCG CAG AGC GCG GGT CGT ATC GTT TCG TTC GAC GCC GCC	642
Ala Ser Asp Pro Gln Ser Ala Gly Arg Ile Val Ser Phe Asp Ala Ala	
115 120 125	
GCG GGT TGG AAC ATC GAG GAA GAG GGC TAT CAG GCG GTG GCG TCG GGT	690
Gly Gly Trp Asn Ile Glu Glu Gly Tyr Gln Ala Val Gly Ser Gly	
130 135 140	
TCG CTG TTC GCG AAG TCG TCG ATG AAG AAG TTG TAT TCG CAG GTT ACC	738
Ser Leu Phe Ala Lys Ser Ser Met Lys Lys Leu Tyr Ser Gln Val Thr	
145 150 155	
GAC GGT GAT TCG GGG CTG CCG GTG GCG GTC GAG GCG CTC TAC GAC GCC	786
Asp Gly Asp Ser Gly Leu Arg Val Ala Val Glu Ala Leu Tyr Asp Ala	
160 165 170 175	
GCC GAC GAC GAC TCC GCC ACC GGC GGT CCG GAC CTG GTG CCG GCC ATC	834
Ala Asp Asp Asp Ser Ala Thr Gly Gly Pro Asp Leu Val Arg Gly Ile	
180 185 190	
TTT CCG ACG GCG GTG ATC ATC GAC GCC GAC GCG GCG GTT GAC GTG CCG	882
Phe Pro Thr Ala Val Ile Ile Asp Ala Asp Gly Ala Val Asp Val Pro	
195 200 205	
GAG AGC CCG ATT GCC GAA TTG GCC CCG GCG ATC ATC GAA AGC CGT TCG	930
Glu Ser Arg Ile Ala Glu Leu Ala Arg Ala Ile Ile Glu Ser Arg Ser	
210 215 220	
GGT GCG GAT ACT TTC GGC TCC GAT GGC GGT GAG AAG TGAGTTTTCG GTATTT	982
Gly Ala Asp Thr Phe Gly Ser Asp Gly Gly Glu Lys	
225 230 235	
CATCTCGCCT GAGCAGGC	1000

(2) INFORMATION FOR SEQ ID NO: 50:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 291 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal
- (ix) FEATURE:

- (A) NAME/KEY: Signal Sequence
- (B) LOCATION: 1...56

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(D) OTHER INFORMATION:

[xi] PROVENANCE DESCRIPTION: SRO ID NO: 58.

Met	Thr	Trp	Pro	Leu	Pro	Asp	Arg	Leu	Ser	Ile	Asn	Ser	Leu	Ser	Gly	
-55						-50					-45					
Thr	Pro	Ala	Val	Asp	Leu	Ser	Ser	Phe	Thr	Asp	Phe	Leu	Arg	Arg	Gln	
-48					-35					-30					-25	
Ala	Pro	Glu	Leu	Leu	Pro	Ala	Ser	Ile	Ser	Gly	Gly	Ala	Pro	Leu	Ala	
			-20						-15					-10		
Gly	Gly	Asp	Ala	Gln	Leu	Pro	His	Gly	Thr	Thr	Ile	Val	Ala	Leu	Lys	
		-5						1				5				
Tyr	Pro	Gly	Gly	Val	Val	Met	Ala	Gly	Asp	Arg	Arg	Ser	Thr	Gln	Gly	
	10					15					20					
Asn	Met	Ile	Ser	Gly	Arg	Asp	Val	Arg	Lys	Val	Tyr	Ile	Thr	Asp	Asp	
25					30					35					40	
Tyr	Thr	Ala	Thr	Gly	Ile	Ala	Gly	Thr	Ala	Ala	Val	Ala	Val	Glu	Phe	
			45						50					55		
Ala	Arg	Leu	Tyr	Ala	Val	Glu	Leu	Glu	His	Tyr	Gln	Lys	Leu	Glu	Gly	
		60						65					70			
Val	Pro	Leu	Thr	Phe	Ala	Gly	Lys	Ile	Asn	Arg	Leu	Ala	Ile	Met	Val	
	75						80					85				
Arg	Gly	Asn	Leu	Ala	Ala	Ala	Met	Gln	Gly	Leu	Leu	Ala	Leu	Pro	Leu	
	90					95					100					
Leu	Ala	Gly	Tyr	Asp	Ile	His	Ala	Ser	Asp	Pro	Gln	Ser	Ala	Gly	Arg	
105					110					115					120	
Ile	Val	Ser	Phe	Asp	Ala	Ala	Gly	Gly	Trp	Asn	Ile	Glu	Glu	Glu	Gly	
		125							130					135		
Tyr	Gln	Ala	Val	Gly	Ser	Gly	Ser	Leu	Phe	Ala	Lys	Ser	Ser	Met	Lys	
		140						145						150		
Lys	Leu	Tyr	Ser	Gln	Val	Thr	Asp	Gly	Asp	Ser	Gly	Leu	Arg	Val	Ala	
	155						160					165				
Val	Glu	Ala	Leu	Tyr	Asp	Ala	Ala	Asp	Asp	Asp	Ser	Ala	Thr	Gly	Gly	
	170					175					180					
Pro	Asp	Leu	Val	Arg	Gly	Ile	Phe	Pro	Thr	Ala	Val	Ile	Ile	Asp	Ala	
185					190					195					200	
Asp	Gly	Ala	Val	Asp	Val	Pro	Glu	Ser	Arg	Ile	Ala	Glu	Leu	Ala	Arg	
			205						210					215		
Ala	Ile	Ile	Glu	Ser	Arg	Ser	Gly	Ala	Asp	Thr	Phe	Gly	Ser	Asp	Gly	
		220						225						230		

168

Gly Glu Lys
235

(2) INFORMATION FOR SEQ ID NO: 59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 900 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
(B) LOCATION: 66...808
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

TTGGCCCGCG CGATCATCGA AAGCCGTTGG GGTGCGGATA CTTTCGGCTC CGATGCGGGT	60
GAGAA GTG AGT TTT CCG TAT TTC ATC TCG CCT GAG CAG GCG ATG CCG GAG	120
Met Ser Phe Pro Tyr Phe Ile Ser Pro Glu Gln Ala Met Arg Glu	
1 5 10 15	
CGC ASC GAG TTG GCG CGT AAG GGC ATT GCG CCG GCC AAA AGC GTG GTG	158
Arg Ser Glu Leu Ala Arg Lys Gly Ile Ala Arg Ala Lys Ser Val Val	
20 25 30	
GCG CTG GCC TAT GCC GGT GGT GTG CTG TTC GTC GCG GAG AAT CCG TCG	206
Ala Leu Ala Tyr Ala Gly Gly Val Leu Phe Val Ala Glu Asn Pro Ser	
35 40 45	
CGG TCG CTG CAG AAG ATC AGT GAG CTC TAC GAT CCG GTG GGT TTT GCG	254
Arg Ser Leu Gln Lys Ile Ser Glu Leu Tyr Asp Arg Val Gly Phe Ala	
50 55 60	
GCT GCG GGC AAG TTC AAC GAG TTC GAC AAT TTG CCG CCG GGC GGG ATC	302
Ala Ala Gly Lys Phe Asn Glu Phe Asp Asn Leu Arg Arg Gly Gly Ile	
65 70 75	
CAG TTC GCC GAC ACC CGC GGT TAC GCC TAT GAC CGT CXT GAC GTC ACC	350
Gln Phe Ala Asp Thr Arg Gly Tyr Ala Tyr Asp Arg Arg Asp Val Thr	
80 85 90 95	
GGT CCG CAG TTG GCC AAT GTC TAC GCG CAG ACT CTA GGC ACC ATC TTC	398
Gly Arg Gln Leu Ala Asn Val Tyr Ala Gln Thr Leu Gly Thr Ile Phe	
100 105 110	
ACC GAA CAG GCC AAG CCC TAC GAG GTT GAG TTG TGT GTG CCC GAG GTG	446
Thr Glu Gln Ala Lys Pro Tyr Glu Val Glu Leu Cys Val Ala Glu Val	
115 120 125	
GCG CAT TAC GGC GAG ACG AAA CGC CCT GAG TTG TAT CXT ATT ACC TAC	494
Ala His Tyr Gly Glu Thr Lys Arg Pro Glu Leu Tyr Arg Ile Thr Tyr	
130 135 140	

169

GAC GGG TCG ATC GCC GAC GAG CCG CAT TTC GTG GTG ATG GGC GGC ACC Asp Gly Ser Ile Ala Asp Glu Pro His Phe Val Val Met Gly Gly Thr	542
145 150 155	
ACG GAG CCG ATC GCC AAC GCG CTC AAA GAG TCG TRT GCC GAG AAC GCC Thr Glu Pro Ile Ala Asn Ala Leu Lys Glu Ser Tyr Ala Glu Asn Ala	590
160 165 170 175	
AGC CTG ACC GAC GCC CTG CBT ATC GCG GTC GCT GCA TTG CCG GCC GGC Ser Leu Thr Asp Ala Leu Arg Ile Ala Val Ala Ala Leu Arg Ala Gly	638
180 185 190	
AGT GCC GAC ACC TCG GGT GGT GAT CAA CCC ACC CTT GGC GTG SCC AGC Ser Ala Asp Thr Ser Gly Gly Asp Gln Pro Thr Leu Gly Val Ala Ser	686
195 200 205	
TTA GAG GTG GCC GTT CTC GAT GCC AAC CCG CCA CGG CGC GCG TTC CCG Leu Glu Val Ala Val Leu Asp Ala Asn Arg Pro Arg Arg Ala Phe Arg	734
210 215 220	
CGC ATC ACC GGC TCC GCC CTG CAA GCG TTG CTG GTA GAC CAG GAA AGC Arg Ile Thr Gly Ser Ala Leu Gln Ala Leu Leu Val Asp Gln Glu Ser	782
225 230 235	
CCG CAG TCT GAC GGC GAA TCG TCG GG CTGAGTCCGA AAGTCCGAGC CCGTCTG Pro Gln Ser Asp Gly Glu Ser Ser Gly	836
240 245	
GGACCCCGCT GCGACGTTAA CTGCGCCTAA CCGCGCTCG ACCTGTCGCC GCGCTCTG ACTT	896 900

(3) INFORMATION FOR SEQ ID NO: 60:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 248 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

Met Ser Phe Pro Tyr Phe Ile Ser Pro Glu Gln Ala Met Arg Glu Arg	
1 5 10 15	
Ser Glu Leu Ala Arg Lys Gly Ile Ala Arg Ala Lys Ser Val Val Ala	
20 25 30	
Leu Ala Tyr Ala Gly Gly Val Leu Phe Val Ala Glu Asn Pro Ser Arg	
35 40 45	
Ser Leu Gln Lys Ile Ser Glu Leu Tyr Asp Arg Val Gly Phe Ala Ala	
50 55 60	

170

Ala Gly Lys Phe Asn Glu Phe Asp Asn Leu Arg Arg Gly Gly Ile Gln
 65 70 75 80

Phe Ala Asp Thr Arg Gly Tyr Ala Tyr Asp Arg Arg Asp Val Thr Gly
 85 90 95

Arg Gln Leu Ala Asn Val Tyr Ala Gln Thr Leu Gly Thr Ile Phe Thr
 100 105 110

Glu Gln Ala Lys Pro Tyr Glu Val Glu Leu Cys Val Ala Glu Val Ala
 115 120 125

His Tyr Gly Glu Thr Lys Arg Pro Glu Leu Tyr Arg Ile Thr Tyr Asp
 130 135 140

Gly Ser Ile Ala Asp Glu Pro His Phe Val Val Met Gly Gly Thr Thr
 145 150 155 160

Glu Pro Ile Ala Asn Ala Leu Lys Glu Ser Tyr Ala Glu Asn Ala Ser
 165 170 175

Leu Thr Asp Ala Leu Arg Ile Ala Val Ala Ala Leu Arg Ala Gly Ser
 180 185 190

Ala Asp Thr Ser Gly Gly Asp Gln Pro Thr Leu Gly Val Ala Ser Leu
 195 200 205

Glu Val Ala Val Leu Asp Ala Asn Arg Pro Arg Arg Ala Phe Arg Arg
 210 215 220

Ile Thr Gly Ser Ala Leu Gln Ala Leu Leu Val Asp Gln Glu Ser Pro
 225 230 235 240

Gln Ser Asp Gly Glu Ser Ser Gly
 245

(2) INFORMATION FOR SEQ ID NO: 61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1560 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 98...1487
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

GAGTCATTGC GTGTCGGGCG TCATTCCGTA CTATCGGTTG GTCCGACTTG ACCTACTGGG 60
 TCAGGCCGCG GAGCACTCGA CCATTAGGTT AGGGGCC GTG ACC CAC TAT GAC GTC 115
 Met Thr His Tyr Asp Val
 3 5

GTC GTT CTC GGA GCC GGT CCC GGC GGG TAT GTC GCG GCG ATT CGC GCC	163
Val Val Leu Gly Ala Gly Pro Gly Tyr Val Ala Ala Ile Arg Ala	
10 15 20	
GCA CAG CTC GGC CTG AGC ACT GCA ATC GTC GAA CCC AAG TAC TGG GGC	211
Ala Gln Leu Gly Leu Ser Thr Ala Ile Val Glu Pro Lys Tyr Trp Gly	
25 30 35	
GGA GTA TGC CTC AAT GTC GGC TGT ATC CCA TCC AAG GCG CTG TTG CGC	259
Gly Val Cys Leu Asn Val Gly Cys Ile Pro Ser Lys Ala Leu Leu Arg	
40 45 50	
AAC GCC GAA CTG GTC CAC ATC TTC ACC AAG GAC GCC AAA GCA TTT GGC	307
Asn Ala Glu Leu Val His Ile Phe Thr Lys Asp Ala Lys Ala Phe Gly	
55 60 65 70	
ATC AGC GGC GAG GTG ACC TTC GAC TAC GGC ATC GCC TAT GAC CGC AGC	355
Ile Ser Gly Glu Val Thr Phe Asp Tyr Gly Ile Ala Tyr Asp Arg Ser	
75 80 85	
CGA AAG GTA GCC GAG GGC AGG GTG GCC GGT GTG CAC TTC CTG ATG AAG	403
Arg Lys Val Ala Glu Gly Arg Val Ala Gly Val His Phe Leu Met Lys	
90 95 100	
AAG AAC AAG ATC ACC GAG ATC CAC GGG TAC GGC ACA TTT GCC GAC GCC	451
Lys Asn Lys Ile Thr Glu Ile His Gly Tyr Gly Thr Phe Ala Asp Ala	
105 110 115	
AAC ACU TTG TTG GTT GAT CTC AAC GAC GGC GGT ACA GAA TCG GTC ACG	499
Asn Thr Leu Leu Val Asp Leu Asn Asp Gly Gly Thr Glu Ser Val Thr	
120 125 130	
TTC GAC AAC GCC ATC ATC GCG ACC GGC AGT AGC ACC CGG CTG GTT CCC	547
Phe Asp Asn Ala Ile Ile Ala Thr Gly Ser Ser Thr Arg Leu Val Pro	
135 140 145 150	
GGC ACC TCA CTG TCG GCC AAC GTA GTC ACC TAC GAG GAA CAG ATC CTG	595
Gly Thr Ser Leu Ser Ala Asn Val Val Thr Tyr Glu Glu Gln Ile Leu	
155 160 165	
TCC CGA GAG CTG CCG AAA TCG ATC ATT ATT GGC GGA GCT GGT GCC ATT	643
Ser Arg Glu Leu Pro Lys Ser Ile Ile Ile Ala Gly Ala Gly Ala Ile	
170 175 180	
GGC ATG GAG TTC GGC TAC GTG CTG AAG AAC TAC GGC GTT GAC GTG ACC	691
Gly Met Glu Phe Gly Tyr Val Leu Lys Asn Tyr Gly Val Asp Val Thr	
185 190 195	
ATC GTG GAA TTC CTT CCG CCG GCG CTG CCC AAC GAG GAC GCC GAT GTG	739
Ile Val Glu Phe Leu Pro Arg Ala Leu Pro Asn Glu Asp Ala Asp Val	
200 205 210	
TCC AAG GAG ATC GAG AAG CAG TTC AAA AAG CTG GGT GTC ACG ATC CTG	787
Ser Lys Glu Ile Glu Lys Gln Phe Lys Lys Leu Gly Val Thr Ile Leu	
215 220 225 230	
ACC GCC ACG AAG GTC GAG TCC ATC GGC GAT GGC GGG TCG CAG GTC ACC	835
Thr Ala Thr Lys Val Glu Ser Ile Ala Asp Gly Gly Ser Gln Val Thr	

172

235										240										245										
GTG ACC GTC ACC AAG GAC GGC GTG GCG CAA GAG CTT AAG GCG GAA AAG	883																													
Val Thr Val Thr Lys Asp Gly Val Ala Gln Glu Leu Lys Ala Glu Lys																														
250	255	260																												
GTG TTG CAG GCC ATC GGA TTT GCG CCC AAC GTC GAA GCG TAC GGG CTG	931																													
Val Leu Gln Ala Ile Gly Phe Ala Pro Asn Val Glu Gly Tyr Gly Leu																														
265	270	275																												
GAC AAG GCA GGC GTC GCG CTG ACC GAC GCG AAG GCT ATC GGT GTC GAC	979																													
Asp Lys Ala Gly Val Ala Leu Thr Asp Arg Lys Ala Ile Gly Val Asp																														
280	285	290																												
GAC TAC ATG GGT ACC AAC GTG GGC CAC ATC TAC GCT ATC GGC GAT GTC	1027																													
Asp Tyr Met Arg Thr Asn Val Gly His Ile Tyr Ala Ile Gly Asp Val																														
295	300	305																												
AAT GGA TTA CTG CAG CTG GCG CAC GTC GCC GAG GCA CAA GGC GTG GTA	1075																													
Asn Gly Leu Leu Gln Leu Ala His Val Ala Glu Ala Gln Gly Val Val																														
315	320	325																												
GCC GCC GAA ACC ATT GCC GGT GCA GAS ACT TTG ACG CTG GGC GAC CAT	1123																													
Ala Ala Glu Thr Thr Ile Ala Gly Ala Glu Thr Leu Thr Leu Gly Asp His																														
330	335	340																												
CGG ATG TTG CCG CCG GCG ACG TTC TGT CAG CCA AAC GTT GCC AGC TTC	1171																													
Arg Met Leu Pro Arg Ala Thr Phe Cys Gln Pro Asn Val Ala Ser Phe																														
345	350	355																												
GGG CTC ACC GAG CAG CAA GCC GCG AAC GAA GGT TAC GAC GTG GTG GTG	1219																													
Gly Leu Thr Gln Gln Gln Ala Arg Asn Glu Gly Tyr Asp Val Val Val																														
360	365	370																												
GCC AAG TTC CCG TTC ACG GCC AAC GCT AAG GCG CAC GGC GTG GGT GAC	1267																													
Ala Lys Phe Pro Phe Thr Ala Asn Ala Lys Ala His Gly Val Gly Asp																														
375	380	385																												
CCC AGT GGG TTC GTC AAG CTG GTG GCC GAC GCC AAG CAC GGC GAG CTA	1315																													
Pro Ser Gly Phe Val Lys Leu Val Ala Asp Ala Lys His Gly Glu Leu																														
395	400	405																												
CTG GGT GCG CAC CTG GTC GGC CAC GAC GTG GCC GAG CTG CTG CCG GAG	1363																													
Leu Gly Gly His Leu Val Gly His Asp Val Ala Glu Leu Leu Pro Glu																														
410	415	420																												
CTC ACG CTG GCG CAG AGG TGG GAC CTG ACC GCC AGC GAG CTG GCT CGC	1411																													
Leu Thr Leu Ala Gln Arg Trp Asp Leu Thr Ala Ser Glu Leu Ala Arg																														
425	430	435																												
AAC CTC CAC ACC CAC CCA ACG ATG TCT GAG GCG CTG CAG GAG TGC TTC	1459																													
Asn Val His Thr His Pro Thr Met Ser Glu Ala Leu Gln Glu Cys Phe																														
440	445	450																												
CAC GGC CTG GTT GGC CAC ATG ATC AAT T TCTGAGCGCG TCATGACGAG CGCGG	1512																													
His Gly Leu Val Gly His Met Ile Asn Phe																														
455	460																													

CGAGCACTGA CACCCCCAG ATCATCATGG GTGCCATCGG TGTGTGTGG

1560

(2) INFORMATION FOR SEQ ID NO: 62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 464 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

```

Met Thr His Tyr Asp Val Val Val Leu Gly Ala Gly Pro Gly Gly Tyr
 1           5           10           15
Val Ala Ala Ile Arg Ala Ala Gln Leu Gly Leu Ser Thr Ala Ile Val
 20           25           30
Glu Pro Lys Tyr Trp Gly Gly Val Cys Leu Asn Val Gly Cys Ile Pro
 35           40           45
Ser Lys Ala Leu Leu Arg Asn Ala Glu Leu Val His Ile Phe Thr Lys
 50           55           60
Asp Ala Lys Ala Phe Gly Ile Ser Gly Glu Val Thr Phe Asp Tyr Gly
 65           70           75           80
Ile Ala Tyr Asp Arg Ser Arg Lys Val Ala Glu Gly Arg Val Ala Gly
 85           90           95
Val His Phe Leu Met Lys Lys Asn Lys Ile Thr Glu Ile His Gly Tyr
100           105           110
Gly Thr Phe Ala Asp Ala Asn Thr Leu Leu Val Asp Leu Asn Asp Gly
115           120           125
Gly Thr Glu Ser Val Thr Phe Asp Asn Ala Ile Ile Ala Thr Gly Ser
130           135           140
Ser Thr Arg Leu Val Pro Gly Thr Ser Leu Ser Ala Asn Val Val Thr
145           150           155           160
Tyr Glu Glu Gln Ile Leu Ser Arg Glu Leu Pro Lys Ser Ile Ile Ile
165           170           175
Ala Gly Ala Gly Ala Ile Gly Met Glu Phe Gly Tyr Val Leu Lys Asn
180           185           190
Tyr Gly Val Asp Val Thr Ile Val Glu Phe Leu Pro Arg Ala Leu Pro
195           200           205
Asn Glu Asp Ala Asp Val Ser Lys Glu Ile Glu Lys Gln Phe Lys Lys
210           215           220
Leu Gly Val Thr Ile Leu Thr Ala Thr Lys Val Glu Ser Ile Ala Asp
225           230           235           240
Gly Gly Ser Gln Val Thr Val Thr Val Thr Lys Asp Gly Val Ala Gln
245           250           255
Glu Leu Lys Ala Glu Lys Val Leu Gln Ala Ile Gly Phe Ala Pro Asn
260           265           270
Val Glu Gly Tyr Gly Leu Asp Lys Ala Gly Val Ala Leu Thr Asp Arg
275           280           285
Lys Ala Ile Gly Val Asp Asp Tyr Met Arg Thr Asn Val Gly His Ile
290           295           300
Tyr Ala Ile Gly Asp Val Asn Gly Leu Leu Gln Leu Ala His Val Ala
305           310           315           320
Glu Ala Gln Gly Val Val Ala Ala Glu Thr Ile Ala Gly Ala Glu Thr
325           330           335
Leu Thr Leu Gly Asp His Arg Met Leu Pro Arg Ala Thr Phe Cys Gln

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174

340	345	350
Pro Asn Val Ala Ser Phe Gly Leu Thr Glu Gln Gln Ala Arg Asn Glu		
355	360	365
Gly Tyr Asp Val Val Val Ala Lys Phe Pro Phe Thr Ala Asn Ala Lys		
370	375	380
Ala His Gly Val Gly Asp Pro Ser Gly Phe Val Lys Leu Val Ala Asp		
385	390	395
Ala Lys His Gly Glu Leu Leu Gly Gly His Leu Val Gly His Asp Val		
405	410	415
Ala Glu Leu Leu Pro Glu Leu Thr Leu Ala Gln Arg Tyr Asp Leu Thr		
420	425	430
Ala Ser Glu Leu Ala Arg Asn Val His Thr His Pro Thr Met Ser Glu		
435	440	445
Ala Leu Gln Glu Cys Phe His Gly Leu Val Gly His Met Ile Asn Phe		
450	455	460

(2) INFORMATION FOR SEQ ID NO: 63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 550 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 101...490
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

GGCCCGCTC GGGCCGCCC TGCAGGAAA GAAGCCCTC CCAGCCCCAG ACTCAGCGA	60
GTATCACC CCATACCCAC ACCAGGAAG ACCGCCATC ATG CCA AAG CTC TCC	115
	Met Ala Lys Leu Ser
	1 5
ACC GAC GAA CTG CTG GAC GCG TTC AAG GAA ATG ACC CTG TTG GAG CTC	163
Thr Asp Glu Leu Leu Asp Ala Phe Lys Glu Met Thr Leu Leu Glu Leu	
	10 15 20
TCC GAC TTC GTC AAG AAG TTC GAG GAG ACC TTC GAG GTC ACC GCC GCC	211
Ser Asp Phe Val Lys Lys Phe Glu Glu Thr Phe Glu Val Thr Ala Ala	
	25 30 35
GCT CCA GTC GCC GTC GCC GCC GCC GGT GCG GCC CCG GCC GGT GCC GCC	259
Ala Pro Val Ala Val Ala Ala Ala Gly Ala Ala Pro Ala Gly Ala Ala	
	40 45 50
GTC GAG GCT GCC GAG GAG CAG TCC GAG TTC GAG GCG ATC CTT GAG GCC	307
Val Glu Ala Ala Glu Glu Gln Ser Glu Phe Asp Val Ile Leu Glu Ala	
	55 60 65
GCC GGC GAC AAG AAG ATC GGC GTC ATC AAG GTG GTC CCG GAG ATC GTT	355
Ala Gly Asp Lys Lys Ile Gly Val Ile Lys Val Val Arg Glu Ile Val	
	70 75 80 85

175

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TCC GGC CTG GGC CTC AAG GAG GCC AAG GAC CTG GTC GAC GGC GCG CCC      403
Ser Gly Leu Gly Leu Lys Glu Ala Lys Asp Leu Val Asp Gly Ala Pro
          95                      95                      100

AAG CCG CTG CTG GAG AAG GTC GCC AAG GAG GCC GCC GAC GAG GCC AAG      451
Lys Pro Leu Leu Glu Lys Val Ala Lys Glu Ala Ala Asp Glu Ala Lys
          105                      110                      115

GCC AAG CTG GAG GCC GCC GGC GCC ACC GTC ACC GTC AAG TAGCTCTGCC CA      502
Ala Lys Leu Glu Ala Ala Gly Ala Thr Val Thr Val Lys
          120                      125                      130

GCGTGTTCTT TTGCTCTGCG TCGGCCCGTA GCGAACACTG CGCCCGCT      550

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(2) INFORMATION FOR SEQ ID NO: 64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iv) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

```

Met Ala Lys Leu Ser Thr Asp Glu Leu Leu Asp Ala Phe Lys Glu Met
  1              5              10              15

Thr Leu Leu Glu Leu Ser Asp Phe Val Lys Lys Phe Glu Glu Thr Phe
  20              25              30

Glu Val Thr Ala Ala Ala Pro Val Ala Val Ala Ala Gly Ala Ala
  35              40              45

Pro Ala Gly Ala Ala Val Glu Ala Ala Glu Glu Gln Ser Glu Phe Asp
  50              55              60

Val Ile Leu Glu Ala Ala Gly Asp Lys Lys Ile Gly Val Ile Lys Val
  65              70              75              80

Val Arg Glu Ile Val Ser Gly Leu Gly Leu Lys Glu Ala Lys Asp Leu
  85              90              95

Val Asp Gly Ala Pro Lys Pro Leu Leu Glu Lys Val Ala Lys Glu Ala
  100             105             110

Ala Asp Glu Ala Lys Ala Lys Leu Glu Ala Ala Gly Ala Thr Val Thr
  115             120             125

Val Lys
  130

```

(2) INFORMATION FOR SEQ ID NO: 65:

(i) SEQUENCE CHARACTERISTICS:

176

(A) LENGTH: 900 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
 (B) LOCATION: 87...770
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

TGAAGCCCAT CGGGTCCAC GAACGACGG CTACCTGATC ACCACGGGGT CTGTAGGGC	60
TCCTCCCCAG GTGATACAGT CGGGCC ATG GCC ATT GAG GGT TCG GTG TTG CGG	112
Met Ala Ile Glu Val Ser Val Leu Arg	
1 5	
GTT TTC ACC GAT TCA GAC GGG AAT TTC GGT AAT CCG CTG GGG GTG ATC	161
Val Phe Thr Asp Ser Asp Gly Asn Phe Gly Asn Pro Leu Gly Val Ile	
10 15 20 25	
AAC GCC AGC AAG GTC GAA CAC CCG GAC AGG CAG CAG CTG GCA GCC CAA	209
Asn Ala Ser Lys Val Glu His Arg Asp Arg Gln Gln Leu Ala Ala Gln	
30 35 40	
TCG GGC TAC AGC GAA ACC ATA TTC GTC GAT CTT CCC AGC CCC GGC TCA	257
Ser Gly Tyr Ser Glu Thr Ile Phe Val Asp Leu Pro Ser Pro Gly Ser	
45 50 55	
ACC ACC GCA CAC GCC ACC ATC CAT ACT CCC CGC ACC GAA ATT CCC TTC	305
Thr Thr Ala His Ala Thr Ile His Thr Pro Arg Thr Glu Ile Pro Phe	
60 65 70	
GCC GGA CAC CCG ACC GTG GGA CGC TCC TGG TGG CTG CCG GAG AGG GGG	353
Ala Gly His Pro Thr Val Gly Ala Ser Trp Trp Leu Arg Glu Arg Gly	
75 80 85	
ACG CCA ATT AAC ACG CTG CAG GTG CCG GCC GGC ATC GTC CAG CTG AGC	401
Thr Pro Ile Asn Thr Leu Gln Val Pro Ala Gly Ile Val Gln Val Ser	
90 95 100 105	
TAC CAC GGT GAT CTC ACC GCC ATC AGC GCC CGC TCG GAA TGG GCA CCC	449
Tyr His Gly Asp Leu Thr Ala Ile Ser Ala Arg Ser Glu Trp Ala Pro	
110 115 120	
GAG TTC GCC ATC CAC GAC CTG GAT TCA CTT GAT GCG CTT GCC GCC GGC	497
Glu Phe Ala Ile His Asp Leu Asp Ser Leu Asp Ala Leu Ala Ala Ala	
125 130 135	
GAC CCC GCC GAC TTT CCG GAC GAC ATC GCG CAC TAC CTC TGG ACC TGG	545
Asp Pro Ala Asp Phe Pro Asp Asp Ile Ala His Tyr Leu Trp Thr Trp	
140 145 150	
ACC GAC CGC TCC GCT GGC TCG CTG CGC GCC CGC ATG TTT GCC GCC AAC	593
Thr Asp Arg Ser Ala Gly Ser Leu Arg Ala Arg Met Phe Ala Ala Asn	

177

155	160	165	
TTG GGC GTC ACC GAA GAC GAA GCG ACC GGT GCG GCG GCC ATC CGG ATT			641
Leu Gly Val Thr Glu Asp Glu Ala Thr Gly Ala Ala Ala Ile Arg Ile			
170	175	180	185
ACC GAT TAC CTC AGC CGT GAC CTC ACC ATC ACC CAG GGC AAA GGA TCG			689
Thr Asp Tyr Leu Ser Arg Asp Leu Thr Ile Thr Gln Gly Lys Gly Ser			
190	195	200	
TTG ATC CAC ACC ACC TGG AGT CCC GAG GGC TGG GTT CGG GTA GCC GGC			737
Leu Ile His Thr Thr Trp Ser Pro Glu Gly Trp Val Arg Val Ala Gly			
205	210	215	
CGA GTT GTC AGC GAC GGT GTG GCA CAA CTC GAC TGACGTAGAG CTCAGCGCTG			796
Arg Val Val Ser Asp Gly Val Ala Gln Leu Asp			
220	225		
CGGATGCAAC ACGCGGSCAA GGTGATCTTG CAGGGGTTGC CCGACCGCGC GCATCTGCAA			850
CGAGTACGAA AGCTCGTGGC COTCGATGCG GTAGGAACGG TCAAGGGCGG			900

(2) INFORMATION FOR SEQ ID NO: 66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 220 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

Met Ala Ile Glu Val Ser Val Leu Arg Val Phe Thr Asp Ser Asp Gly		
1	5	10
Asn Phe Gly Asn Pro Leu Gly Val Ile Asn Ala Ser Lys Val Gln His		
20	25	30
Arg Asp Arg Gln Gln Leu Ala Ala Gln Ser Gly Tyr Ser Glu Thr Ile		
35	40	45
Phe Val Asp Leu Pro Ser Pro Gly Ser Thr Thr Ala His Ala Thr Ile		
50	55	60
His Thr Pro Arg Thr Glu Ile Pro Phe Ala Gly His Pro Thr Val Gly		
65	70	75
Ala Ser Trp Trp Leu Arg Glu Arg Gly Thr Pro Ile Asn Thr Leu Gln		
85	90	95
Val Pro Ala Gly Ile Val Gln Val Ser Tyr His Gly Asp Leu Thr Ala		
100	105	110
Ile Ser Ala Arg Ser Glu Trp Ala Pro Glu Phe Ala Ile His Asp Leu		

178

115	120	125
Asp Ser Leu Asp Ala Leu Ala Ala Ala Asp Pro Ala Asp Phe Pro Asp		
130	135	140
Asp Ile Ala His Tyr Leu Trp Thr Trp Thr Asp Arg Ser Ala Gly Ser		
145	150	155
Leu Arg Ala Arg Met Phe Ala Ala Asn Leu Gly Val Thr Glu Asp Glu		
165	170	175
Ala Thr Gly Ala Ala Ala Ile Arg Ile Thr Asp Tyr Leu Ser Arg Asp		
180	185	190
Leu Thr Ile Thr Gln Gly Lys Gly Ser Leu Ile His Thr Thr Trp Ser		
195	200	205
Pro Glu Gly Trp Val Arg Val Ala Gly Arg Val Val Ser Asp Gly Val		
210	215	220
Ala Gln Leu Asp		
225		

(2) INFORMATION FOR SEQ ID NO: 67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 500 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 49...465
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

GTTTGTGGTG TCGGTGGTCT GGGGGGCGCC AACTGGGATT CGGTGGG GTG GGT GCA	57
Met Gly Ala	
1	
GGT CCG GCG ATG GGC ATC GGA GGT GTG GGT GGT TTG GGT GGG GCC GGT	105
Gly Pro Ala Met Gly Ile Gly Gly Val Gly Gly Leu Gly Gly Ala Gly	
5 10 15	
TCG GGT CCG GCG ATG GGC ATG GGG GGT GTG GGT GGT TTG GGT GGG GCC	153
Ser Gly Pro Ala Met Gly Met Gly Gly Val Gly Gly Leu Gly Gly Ala	
20 25 30 35	
GGT TCG GGT CCG GCG ATG GGC ATG GGG GGT GTG GGT GGT TTA GAT GCG	201
Gly Ser Gly Pro Ala Met Gly Met Gly Gly Val Gly Gly Leu Asp Ala	
40 45 50	
GCC GGT TCG GGC GAG GGC GGC TCT CCT GCG GCG ATC GGC ATC GGA GTT	249

179

Ala Gly Ser Gly Glu Gly Gly Ser Pro Ala Ala Ile Gly Ile Gly Val	
55 60 65	
GGC GGA GGC GGA GGT GGG GGT GGG GGT GGC GGC GGC GGC GCC GAC ACG	297
Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Ala Asp Thr	
70 75 80	
AAC CGC TCC GAC AGG TCG TCG GAC GTC GGG GGC GGA GTC TGG CCG TTG	345
Asn Arg Ser Asp Arg Ser Ser Asp Val Gly Gly Val Trp Pro Leu	
85 90 95	
GGC TTC GGT ACG TTT GCC GAT GCG GGC GCC GGC GGA AAC GAA GCA CTG	393
Gly Phe Gly Arg Phe Ala Asp Ala Gly Ala Gly Gly Asn Glu Ala Leu	
100 105 110 115	
GGG TCG AAG AAC GGC TGC GCT GCC ATA TCG TCC GGA GCT TCC ATA CCT	441
Gly Ser Lys Asn Gly Cys Ala Ala Ile Ser Ser Gly Ala Ser Ile Pro	
120 125 130	
TCG TGC GGC GGG AAG AGC TTG TCG TATCTCGCCG CCGTGACAAC CTCTCAGAGT	495
Ser Cys Gly Arg Lys Ser Leu Ser	
135	
GGCGCT	500

(2) INFORMATION FOR SEQ ID NO: 68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iv) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

Met Gly Ala Gly Pro Ala Met Gly Ile Gly Gly Val Gly Gly Leu Gly	
1 5 10 15	
Gly Ala Gly Ser Gly Pro Ala Met Gly Met Gly Gly Val Gly Gly Leu	
20 25 30	
Gly Gly Ala Gly Ser Gly Pro Ala Met Gly Met Gly Gly Val Gly Gly	
35 40 45	
Leu Asp Ala Ala Gly Ser Gly Glu Gly Gly Ser Pro Ala Ala Ile Gly	
50 55 60	
Ile Gly Val Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly	
65 70 75 80	
Ala Asp Thr Asn Arg Ser Asp Arg Ser Ser Asp Val Gly Gly Gly Val	
85 90 95	
Trp Pro Leu Gly Phe Gly Arg Phe Ala Asp Ala Gly Ala Gly Gly Asn	

180

100	105	110
Glu Ala Leu Gly Ser Lys Asn Gly Cys Ala Ala Ile Ser Ser Gly Ala		
115	120	125
Ser Ile Pro Ser Cys Gly Arg Lys Ser Leu Ser		
130	135	

(2) INFORMATION FOR SEQ ID NO: 69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2050 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 22...2019
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

AGGCGACTCT GAGAGGTGT C ATG GCG GCC GAC TAC GAC AAG CTC TTC CGG	51
Met Ala Ala Asp Tyr Asp Lys Leu Phe Arg	
1 5 10	
CCG CAC GAA GGT ATG GAA GCT CCG GAC GAT ATG GCA GCG CAG CCG TTC	99
Pro His Glu Gly Met Glu Ala Pro Asp Asp Met Ala Ala Gln Pro Phe	
15 20 25	
TTC GAC CCC AGT GCT TCG TTT CCG CCG GCG CCC GCA TCG GCA AAC CTA	147
Phe Asp Pro Ser Ala Ser Phe Pro Pro Ala Pro Ala Ser Ala Asn Leu	
30 35 40	
CCG AAG CCC AAC GGC CAG ACT CCG CCC CCG ACG TCC GAC GAC CTG TCG	195
Pro Lys Pro Asn Gly Gln Thr Pro Pro Pro Thr Ser Asp Asp Leu Ser	
45 50 55	
GAG CCG TTC GTG TCG GCC CCG CCG CCG CCA CCG CCA CCC CCA CCG CCG	243
Glu Arg Phe Val Ser Ala Pro Pro Pro Pro Pro Pro Pro Pro Pro	
60 65 70	
CCT CCG CCA ACT CCG ATG CCG ATC GCC GCA GGA GAG CCG CCC TCG CCG	291
Pro Pro Pro Thr Pro Met Pro Ile Ala Ala Gly Gln Pro Pro Ser Pro	
75 80 85 90	
GAA CCG GCC GCA TCT AAA CCA CCC ACA CCC CCC ATG CCC ATC GCC GGA	339
Glu Pro Ala Ala Ser Lys Pro Pro Thr Pro Pro Met Pro Ile Ala Gly	
95 100 105	
CCC GAA CCG GCC CCA CCC AAA CCA CCC ACA CCC CCC ATG CCC ATC GCC	387
Pro Glu Pro Ala Pro Pro Lys Pro Pro Thr Pro Pro Met Pro Ile Ala	
110 115 120	

181

GGA CCC GAA CCG GCC CCA CCC AAA CCA CCC ACA CCG CCG ATG CCC ATC Gly Pro Glu Pro Ala Pro Pro Lys Pro Pro Thr Pro Pro Met Pro Ile 125 130 135	435
GCC GGA CCG GCA CCC ACC CCA ACC GAA TCC CAG TTG GCG CCC CCC AGA Ala Gly Pro Ala Pro Thr Pro Thr Glu Ser Gln Leu Ala Pro Pro Arg 140 145 150	483
CCA CCG ACA CCA CAA ACG CCA ACC GGA GCG CCG CAG CAA CCG GAA TCA Pro Pro Thr Pro Gln Thr Pro Thr Gly Ala Pro Gln Gln Pro Glu Ser 155 160 165 170	531
CCG GCG CCC CAC GTA CCC TCG CAC GCG CCA CAT CAA CCC CCG CGC ACC Pro Ala Pro His Val Pro Ser His Gly Pro His Gln Pro Arg Arg Thr 175 180 185	579
GCA CCA GCA CCG CCC TGG GCA AAG ATG CCA ATC GGC GAA CCC CCG CCC Ala Pro Ala Pro Pro Trp Ala Lys Met Pro Ile Gly Glu Pro Pro Pro 190 195 200	627
GCT CCG TCC AGA CCG TCT GCG TCC CCG GCC GAA CCA CCG ACC CCG CCG Ala Pro Ser Arg Pro Ser Ala Ser Pro Ala Glu Pro Pro Thr Arg Pro 205 210 215	675
GCC CCC CAA CAC TCC CGA CGT GCG CGC CCG GGT CAC CGC TAT CGC ACA Ala Pro Gln His Ser Arg Ala Arg Arg Gly His Arg Tyr Arg Thr 220 225 230	723
GAC ACC GAA CGA AAC GTC GGG AAG GTA GCA ACT GGT CCA TCC ATC CAG Asp Thr Glu Arg Asn Val Gly Lys Val Ala Thr Gly Pro Ser Ile Gln 235 240 245 250	771
GCG CCG CTG CCG GCA GAG GAA GCA TCC GGC GCG CAG CTC GCC CCC GGA Ala Arg Leu Arg Ala Glu Glu Ala Ser Gly Ala Gln Leu Ala Pro Gly 255 260 265	819
AAG GAG CCC TCG CCA GCG CCG TTG GGC CAA CCG AGA TCG TAT CTG GGT Thr Glu Pro Ser Pro Ala Pro Leu Gly Gln Pro Arg Ser Tyr Leu Ala 270 275 280	867
CCG CCC ACC CGC CCC GCG CCG ACA GAA CCT CCC CCC AGC CCC TCG CCG Pro Pro Thr Arg Pro Ala Pro Thr Glu Pro Pro Pro Ser Pro Ser Pro 285 290 295	915
CAG CGC AAC TCC GGT CCG CGT GCC GAG CGA CGC GTC CAC CCC GAT TTA Gln Arg Asn Ser Gly Arg Arg Ala Glu Arg Arg Val His Pro Asp Leu 300 305 310	963
GCC GCC CAA CAT GCC GCG GCG CAA CCT GAT TCA ATT ACG GCC GCA ACC Ala Ala Gln His Ala Ala Ala Gln Pro Asp Ser Ile Thr Ala Ala Thr 315 320 325 330	1011
ACT GCG GGT CGT CGC CGC AAG CGT GCA GCG CCG GAT CTG GAC GCG ACA Thr Gly Gly Arg Arg Lys Arg Ala Ala Pro Asp Leu Asp Ala Thr 335 340 345	1059
CAG AAA TCC TTA AAG CCG GCG GCC AAG GGG CCG AAG GTG AAG AAG GTG Gln Lys Ser Leu Arg Pro Ala Ala Lys Gly Pro Lys Val Lys Lys Val 350 355 360 365	1107

350				355				360				
AAG CCC CAG AAA CCG	AAG GCC ACG	AAG CCG CCC AAA GTG	GTG TCG CAG									1155
Lys Pro Gln Lys Pro	Lys Ala Thr	Lys Pro Pro Lys Val Val	Ser Gln									
365	370	375										
CGC GGC TGG CGA CAT	TGG GTG CAT	GGC TTG ACG CGA ATC	AAC CTG GGC									1203
Arg Gly Trp Arg His	Trp Val His	Ala Leu Thr Arg Ile	Asn Leu Gly									
380	385	390										
CTG TCA CCC GAC GAG	AAG TAC GAG	CTG GAC CTG CAC GCT	CGA GTC CGC									1251
Leu Ser Pro Asp Glu	Lys Tyr Glu Leu	Asp Leu His Ala Arg	Val Arg									
395	400	405	410									
CGC AAT CCC CGC GGG	TCG TAT CAG ATC	GCC GTC GTC GGT	CTC AAA GGT									1299
Arg Asn Pro Arg Gly	Ser Tyr Gln Ile	Ala Val Val Gly	Leu Lys Gly									
415	420	425										
GGG GCT GGC AAA ACC	ACG CTG ACA GCA GCG	TTG GGG TCG ACG	TTG GCT									1347
Gly Ala Gly Lys Thr	Thr Leu Thr Ala	Ala Leu Gly Ser	Thr Leu Ala									
430	435	440										
CAG GTG CCG GCC GAC	CGG ATC CTG	GCT CTA GAC GCG	GAT CCA GGC GCC									1395
Gln Val Arg Ala Asp	Arg Ile Leu	Ala Leu Asp Ala	Asp Pro Gly Ala									
445	450	455										
CGA AAC CTC GCC GAT	CGG GTA GGG	CGA CAA TCG GGC	GCG ACC ATC GCT									1443
Gly Asn Leu Ala Asp	Arg Val Gly Arg	Gln Ser Gly Ala	Thr Ile Ala									
460	465	470										
GAT GTG CTT GCA GAR	AAA GAG CTG	TCG CAC TAC AAC	GAC ATC CGC GCA									1491
Asp Val Leu Ala Glu	Lys Glu Leu Ser	His Tyr Asn Asp	Ile Arg Ala									
475	480	485	490									
CAC ACT AGC GTC AAT	GCG GTC AAT	CTG GAA GTG	CTG CCG GCA CCG									1539
His Thr Ser Val Asn	Ala Val Asn	Leu Glu Val Leu	Pro Ala Pro Glu									
495	500	505										
TAC AGC TCG GCG CAG	CGC GCG CTC	AGC GAC GCC GAC	TGG CAT TTC ATC									1587
Tyr Ser Ser Ala Gln	Arg Ala Leu Ser	Asp Ala Asp	Trp His Phe Ile									
510	515	520										
GCC GAT CGT GCG TCG	AGG TTT TAC	AAC CTC GTC TTG	GCT GAT TGT GGG									1635
Ala Asp Pro Ala Ser	Arg Phe Tyr Asn	Leu Val Leu Ala	Asp Cys Gly									
525	530	535										
GCC GGC TTC TTC GAC	CCG CTG ACC	CGC GGC GTG	CTG TCC ACG GTG									1683
Ala Gly Phe Phe Asp	Pro Leu Thr Arg	Gly Val Leu Ser	Thr Val Ser									
540	545	550										
GGT GTC GTG GTC GTG	GCA AGT GTC	TCA ATC GAC GGC	GCA CAA CAG GCG									1731
Gly Val Val Val Val	Ala Ser Val Ser	Ile Asp Gly Ala	Gln Gln Ala									
555	560	565	570									
TCG GTC GCG TTG GAC	TGG TTG CGC	AAC AAC GGT	TAC CAA GAT									1779
Ser Val Ala Leu Asp	Trp Leu Arg Asn	Asn Gly Tyr	Gln Asp Leu Ala									
575	580	585										

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AGC CGC GCA TGC GTG GTC ATC AAT CAC ATC ATG CCG GGA GAA CCC AAT	1827
Ser Arg Ala Cys Val Val Ile Asn His Ile Met Pro Gly Glu Pro Asn	
590 595 600	
GTC GCA GTT AAA GAC CTG GTG CGG CAT TTC GAA CAG CAA GTT CAA CCC	1875
Val Ala Val Lys Asp Leu Val Arg His Phe Glu Gln Gln Val Gln Pro	
605 610 615	
GGC CGG GTC GTG GTC ATG CCG TGG GAC AGG CAC ATT GCG GCC GGA ACC	1923
Gly Arg Val Val Val Met Pro Trp Asp Arg His Ile Ala Ala Gly Thr	
620 625 630	
GAG ATT TCA CTC GAC TTG CTC GAC CCT ATC TAC AAG CGC AAG GTC CTC	1971
Glu Ile Ser Leu Asp Leu Leu Asp Pro Ile Tyr Lys Arg Lys Val Leu	
635 640 645 650	
GAA TTG GCC GCA GCG CTA TCC GAC GAT TTC GAG AGG GCT GGA CGT CGT T	2020
Glu Leu Ala Ala Ala Leu Ser Asp Asp Phe Glu Arg Ala Gly Arg Arg	
655 660 665	
GAGCGCACCT GCTGTGCTG CTGGTCCCTAC	2050

(2) INFORMATION FOR SEQ ID NO: 70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 666 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iv) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

Met	Ala	Ala	Asp	Tyr	Asp	Lys	Leu	Phe	Arg	Pro	His	Glu	Gly	Met	Glu
1					5					10					15
Ala	Pro	Asp	Asp	Met	Ala	Ala	Gln	Pro	Phe	Phe	Asp	Pro	Ser	Ala	Ser
			20					25						30	
Phe	Pro	Pro	Ala	Pro	Ala	Ser	Ala	Asn	Leu	Pro	Lys	Pro	Asn	Gly	Gln
			35					40						45	
Thr	Pro	Pro	Pro	Thr	Ser	Asp	Asp	Leu	Ser	Glu	Arg	Phe	Val	Ser	Ala
	50					55					60				
Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Thr	Pro	Met	
	65					70					75			80	
Pro	Ile	Ala	Ala	Gly	Glu	Pro	Pro	Ser	Pro	Glu	Pro	Ala	Ala	Ser	Lys
				85					90					95	
Pro	Pro	Thr	Pro	Pro	Met	Pro	Ile	Ala	Gly	Pro	Glu	Pro	Ala	Pro	Pro
				100					105					110	
Lys	Pro	Pro	Thr	Pro	Pro	Met	Pro	Ile	Ala	Gly	Pro	Glu	Pro	Ala	Pro

184

115	120	125
Pro Lys Pro Pro Thr	Pro Pro Met Pro Ile Ala Gly Pro Ala Pro Thr	
130	135	140
Pro Thr Glu Ser Gln Leu Ala Pro Pro Arg Pro Pro Thr Pro Gln Thr		
145	150	155
Pro Thr Gly Ala Pro Gln Gln Pro Glu Ser Pro Ala Pro His Val Pro		
165	170	175
Ser His Gly Pro His Gln Pro Arg Arg Thr Ala Pro Ala Pro Pro Trp		
180	185	190
Ala Lys Met Pro Ile Gly Glu Pro Pro Pro Ala Pro Ser Arg Pro Ser		
195	200	205
Ala Ser Pro Ala Glu Pro Pro Thr Arg Pro Ala Pro Gln His Ser Arg		
210	215	220
Arg Ala Arg Arg Gly His Arg Tyr Arg Thr Asp Thr Glu Arg Asn Val		
225	230	235
Gly Lys Val Ala Thr Gly Pro Ser Ile Gln Ala Arg Leu Arg Ala Glu		
245	250	255
Glu Ala Ser Gly Ala Gln Leu Ala Pro Gly Thr Glu Pro Ser Pro Ala		
260	265	270
Pro Leu Gly Gln Pro Arg Ser Tyr Leu Ala Pro Pro Thr Arg Pro Ala		
275	280	285
Pro Thr Glu Pro Pro Pro Ser Pro Ser Pro Gln Arg Asn Ser Gly Arg		
290	295	300
Arg Ala Glu Arg Arg Val His Pro Asp Leu Ala Ala Gln His Ala Ala		
305	310	315
Ala Gln Pro Asp Ser Ile Thr Ala Ala Thr Thr Gly Gly Arg Arg Arg		
325	330	335
Lys Arg Ala Ala Pro Asp Leu Asp Ala Thr Gln Lys Ser Leu Arg Pro		
340	345	350
Ala Ala Lys Gly Pro Lys Val Lys Lys Val Lys Pro Gln Lys Pro Lys		
355	360	365
Ala Thr Lys Pro Pro Lys Val Val Ser Gln Arg Gly Trp Arg His Trp		
370	375	380
Val His Ala Leu Thr Arg Ile Asn Leu Gly Leu Ser Pro Asp Glu Lys		
385	390	395
Tyr Glu Leu Asp Leu His Ala Arg Val Arg Arg Asn Pro Arg Gly Ser		
405	410	415
Tyr Gln Ile Ala Val Val Gly Leu Lys Gly Gly Ala Gly Lys Thr Thr		
420	425	430

185

Leu Thr Ala Ala Leu Gly Ser Thr Leu Ala Gln Val Arg Ala Asp Arg
 435 440 445
 Ile Leu Ala Leu Asp Ala Asp Pro Gly Ala Gly Asn Leu Ala Asp Arg
 450 455 460
 Val Gly Arg Gln Ser Gly Ala Thr Ile Ala Asp Val Leu Ala Glu Lys
 465 470 475 480
 Glu Leu Ser His Tyr Asn Asp Ile Arg Ala His Thr Ser Val Asn Ala
 485 490 495
 Val Asn Leu Glu Val Leu Pro Ala Pro Glu Tyr Ser Ser Ala Gln Arg
 500 505 510
 Ala Leu Ser Asp Ala Asp Trp His Phe Ile Ala Asp Pro Ala Ser Arg
 515 520 525
 Phe Tyr Asn Leu Val Leu Ala Asp Cys Gly Ala Gly Phe Phe Asp Pro
 530 535 540
 Leu Thr Arg Gly Val Leu Ser Thr Val Ser Gly Val Val Val Val Ala
 545 550 555 560
 Ser Val Ser Ile Asp Gly Ala Gln Gln Ala Ser Val Ala Leu Asp Trp
 565 570 575
 Leu Arg Asn Asn Gly Tyr Gln Asp Leu Ala Ser Arg Ala Cys Val Val
 580 585 590
 Ile Asn His Ile Met Pro Gly Glu Pro Asn Val Ala Val Lys Asp Leu
 595 600 605
 Val Arg His Phe Glu Gln Gln Val Gln Pro Gly Arg Val Val Val Met
 610 615 620
 Pro Trp Asp Arg His Ile Ala Ala Gly Thr Glu Ile Ser Leu Asp Leu
 625 630 635 640
 Leu Asp Pro Ile Tyr Lys Arg Lys Val Leu Glu Leu Ala Ala Ala Leu
 645 650 655
 Ser Asp Asp Phe Glu Arg Ala Gly Arg Arg
 660 665

(2) INFORMATION FOR SEQ ID NO: 71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1890 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 79...1861

187

GAG TTC CCC GAC CTT GAG GGG CAG GTT CAA GAT CTG GCC GCC CAG GGG Glu Phe Pro Asp Leu Glu Gly Gln Val Gln Asp Leu Ala Ala Gln Gly 205 210 215	735
CTG GGG TTC GGC GTC CAC GTC ATC ATC TCC ACG CCA CGC TGG ACA GAG Leu Gly Phe Gly Val His Val Ile Ile Ser Thr Pro Arg Trp Thr Glu 220 225 230 235	783
CTG AAG TCG CGT GTT CGC GAC TAC CTC GGC ACC AAG ATC GAG TTC CGG Leu Lys Ser Arg Val Arg Asp Tyr Leu Gly Thr Lys Ile Glu Phe Arg 240 245 250	831
CTT GGT GAC GTC AAT GAA ACC CAG ATC GAC CGG ATT ACC CGC GAG ATC Leu Gly Asp Val Asn Glu Thr Gln Ile Asp Arg Ile Thr Arg Glu Ile 255 260 265	879
CCG GCG AAT CGT CCG GGT CGG GCA GTG TCG ATG GAA AAG CAC CAT CTG Pro Ala Asn Arg Pro Gly Arg Ala Val Ser Met Glu Lys His His Leu 270 275 280	927
ATG ATC GGC GTG CCC AGG TTC GAC GGC GTG CAC AGC GCC GAT AAC CTG Met Ile Gly Val Pro Arg Phe Asp Gly Val His Ser Ala Asp Asn Leu 285 290 295	975
GTG GAG GCG ATC ACC GCG GGG GTG ACG CAG ATC GCT TCC CAG CAC ACC Val Glu Ala Ile Thr Ala Gly Val Thr Gln Ile Ala Ser Gln His Thr 300 305 310 315	1023
GAA CAG GCA CCT CCG GTG CCG GTC CTG CCG GAG CGT ATC CRC CTG CAC Glu Gln Ala Pro Pro Val Arg Val Leu Pro Glu Arg Ile His Leu His 320 325 330	1071
GAA CTC GAC CCG AAC CCG CCG GGA CCA GAG TCC GAC TAC CGC ACT CGC Glu Leu Asp Pro Asn Pro Pro Gly Pro Glu Ser Asp Tyr Arg Thr Arg 335 340 345	1119
TGG GAG ATT CCG ATC GGC TTG CGC GAG ACG GAC CTG ACG CCG GCT CAC Trp Glu Ile Pro Ile Gly Leu Arg Glu Thr Asp Leu Thr Pro Ala His 350 355 360	1167
TGC CAC ATG CAC ACG AAC CCG CAC CTA CTG ATC TTC GGT GCG GCC AAA Cys His Met His Thr Asn Pro His Leu Leu Ile Phe Gly Ala Ala Lys 365 370 375	1215
TGG GGC AAG ACG ACC ATT GCC CAC GCG ATC GCG CGC GCT ATT TGT GCG Ser Gly Lys Thr Thr Ile Ala His Ala Ile Ala Arg Ala Ile Cys Ala 380 385 390 395	1263
CGA AAC AGT CCC CAG CAG GTG CCG TTC AAG CTC GCG GAC TAC CGC TCG Arg Asn Ser Pro Gln Gln Val Arg Phe Met Leu Ala Asp Tyr Arg Ser 400 405 410	1311
GGC CTG CTG GAC GCG GTG CCG GAC ACC CAT CTG CTG GGC GCC GCG GCG Gly Leu Leu Asp Ala Val Pro Asp Thr His Leu Leu Gly Ala Gly Ala 415 420 425	1359
ATC AAC CCG AAC AGC CGC TCG CTA GAC GAG GCC GCT CAA GCA CTG CCG Ile Asn Arg Asn Ser Ala Ser Leu Asp Glu Ala Ala Gln Ala Leu Ala 430 435 440 445	1407

188

430	435	440	
GTC AAC CTG AAG ANG CCG TTG CCG CCG ACC GAC CTG ACG ACG GCG CAG			1455
Val Asn Leu Lys Lys Arg Leu Pro Pro Thr Asp Leu Thr Thr Ala Gln			
445	450	455	
CTA CGC TCG CST TCG TGG TGG ASC GGA TTT GAC GTC GTG CTT CTG GTC			1503
Leu Arg Ser Arg Ser Trp Trp Ser Gly Phe Asp Val Val Leu Leu Val			
465	465	470	475
GAC GAT TGG CAC ATG ATC GTG GGT GCC GCC GCG GCG ATG CCG CCG ATG			1551
Asp Asp Trp His Met Ile Val Gly Ala Ala Gly Gly Met Pro Pro Met			
480	485	490	
GCA CCG CTG GCC CCG TTA TTG CCG GCG GCG GCA GAT ATC GGG TTG CAC			1599
Ala Pro Leu Ala Pro Leu Leu Pro Ala Ala Ala Asp Ile Gly Leu His			
495	500	505	
ATC ATT GTC ACC TGT CAG ATG ASC CAG GCT TAC AAG GCA ACC ATG GAC			1647
Ile Ile Val Thr Cys Gln Met Ser Gln Ala Tyr Lys Ala Thr Met Asp			
510	515	520	
AAG TTC GTC GGC GCC GCA TTC GCG TCG GGC GCT CCG ACA ATG TTC CTT			1695
Lys Phe Val Gly Ala Ala Phe Gly Ser Gly Ala Pro Thr Met Phe Leu			
525	530	535	
TOG GGC GAG AAG CAG GAA TTC CCA TCC AGT GAG TTC AAG GTC AAG CCG			1743
Ser Gly Glu Lys Gln Phe Pro Ser Ser Glu Phe Lys Val Lys Arg			
540	545	550	555
CGC CCC CCT GGC CAG GCA TTT CTC GTC TCG CCA GAC GGC AAA GAG GTC			1791
Arg Pro Pro Gly Gln Ala Phe Leu Val Ser Pro Asp Gly Lys Glu Val			
560	565	570	
ATC CAG GCC CCC TAC ATC GAG CCT CCA GAA GAA GTG TTC GCA GCA CCC			1839
Ile Gln Ala Pro Tyr Ile Glu Pro Pro Glu Glu Val Phe Ala Ala Pro			
575	580	585	
CCA AGC GCC GGT TAAGATTATT TCATTGCCCG TGTATCAGGA CCGAGCTC			1890
Pro Ser Ala Gly			
590			

(2) INFORMATION FOR SEQ ID NO: 72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 591 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

Met	Thr	Ala	Glu	Pro	Glu	Val	Arg	Thr	Leu	Arg	Glu	Val	Val	Leu	Asp
1					5				10					15	

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Gln Leu Gly Thr Ala Glu Ser Arg Ala Tyr Lys Met Trp Leu Pro Pro
 20 25 30
 Leu Thr Asn Pro Val Pro Leu Asn Glu Leu Ile Ala Arg Asp Arg Arg
 35 40 45
 Gln Pro Leu Arg Phe Ala Leu Gly Ile Met Asp Glu Pro Arg Arg His
 50 55 60
 Leu Gln Asp Val Trp Gly Val Asp Val Ser Gly Ala Gly Gly Asn Ile
 65 70 75 80
 Gly Ile Gly Gly Ala Pro Gln Thr Gly Lys Ser Thr Leu Leu Gln Thr
 85 90 95
 Met Val Met Ser Ala Ala Ala Thr His Ser Pro Arg Asn Val Gln Phe
 100 105 110
 Tyr Cys Ile Asp Leu Gly Gly Gly Gly Leu Ile Tyr Leu Glu Asn Leu
 115 120 125
 Pro His Val Gly Gly Val Ala Asn Arg Ser Glu Pro Asp Lys Val Asn
 130 135 140
 Arg Val Val Ala Glu Met Gln Ala Val Met Arg Gln Arg Glu Thr Thr
 145 150 155 160
 Phe Lys Glu His Arg Val Gly Ser Ile Gly Met Tyr Arg Gln Leu Arg
 165 170 175
 Asp Asp Pro Ser Gln Pro Val Ala Ser Asp Pro Tyr Gly Asp Val Phe
 180 185 190
 Leu Ile Ile Asp Gly Trp Pro Gly Phe Val Gly Glu Phe Pro Asp Leu
 195 200 205
 Glu Gly Gln Val Gln Asp Leu Ala Ala Gln Gly Leu Gly Phe Gly Val
 210 215 220
 His Val Ile Ile Ser Thr Pro Arg Trp Thr Glu Leu Lys Ser Arg Val
 225 230 235 240
 Arg Asp Tyr Leu Gly Thr Lys Ile Glu Phe Arg Leu Gly Asp Val Asn
 245 250 255
 Glu Thr Gln Ile Asp Arg Ile Thr Arg Glu Ile Pro Ala Asn Arg Pro
 260 265 270
 Gly Arg Ala Val Ser Met Glu Lys His His Leu Met Ile Gly Val Pro
 275 280 285
 Arg Phe Asp Gly Val His Ser Ala Asp Asn Leu Val Glu Ala Ile Thr
 290 295 300
 Ala Gly Val Thr Gln Ile Ala Ser Gln His Thr Glu Gln Ala Pro Pro
 305 310 315 320
 Val Arg Val Leu Pro Glu Arg Ile His Leu His Glu Leu Asp Pro Asn

190

	325		330		335
Pro Pro Gly	Pro Glu Ser Asp Tyr	Arg Thr Arg Trp	Glu Ile Pro Ile		
	340	345	350		
Gly Leu Arg	Glu Thr Asp Leu Thr	Pro Ala His Cys His Met His Thr			
	355	360	365		
Asn Pro His	Leu Leu Ile Phe Gly Ala Ala Lys Ser Gly Lys Thr Thr				
	370	375	380		
Ile Ala His	Ala Ile Ala Arg Ala Ile Cys Ala Arg Asn Ser Pro Gln				
	385	390	395		400
Gln Val Arg	Phe Met Leu Ala Asp Tyr Arg Ser Gly Leu Leu Asp Ala				
	405	410	415		
Val Pro Asp	Thr His Leu Leu Gly Ala Gly Ala Ile Asn Arg Asn Ser				
	420	425	430		
Ala Ser Leu	Asp Glu Ala Ala Gln Ala Leu Ala Val Asn Leu Lys Lys				
	435	440	445		
Arg Leu Pro	Pro Thr Asp Leu Thr Thr Ala Gln Leu Arg Ser Arg Ser				
	450	455	460		
Trp Trp Ser	Gly Phe Asp Val Val Leu Leu Val Asp Asp Trp His Met				
	465	470	475		480
Ile Val Gly	Ala Ala Gly Gly Met Pro Pro Met Ala Pro Leu Ala Pro				
	485	490	495		
Leu Leu Pro	Ala Ala Ala Asp Ile Gly Leu His Ile Ile Val Thr Cys				
	500	505	510		
Gln Met Ser	Gln Ala Tyr Lys Ala Thr Met Asp Lys Phe Val Gly Ala				
	515	520	525		
Ala Phe Gly	Ser Gly Ala Pro Thr Met Phe Leu Ser Gly Glu Lys Gln				
	530	535	540		
Glu Phe Pro	Ser Ser Glu Phe Lys Val Lys Arg Arg Pro Pro Gly Gln				
	545	550	555		560
Ala Phe Leu	Val Ser Pro Asp Gly Lys Glu Val Ile Gln Ala Pro Tyr				
	565	570	575		
Ile Glu Pro	Pro Glu Glu Val Phe Ala Ala Pro Pro Ser Ala Gly				
	580	585	590		

(2) INFORMATION FOR SEQ ID NO: 73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

191

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

Asp	Pro	Val	Asp	Asp	Ala	Phe	Ile	Ala	Lys	Leu	Asn	Thr	Ala	Gly
1				5					10					15

(2) INFORMATION FOR SEQ ID NO: 74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(ix) Feature:

- (A) NAME/KEY: Other
- (B) LOCATION: 14
- (C) OTHER INFORMATION: Xaa is unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

Asp	Pro	Val	Asp	Ala	Ile	Ile	Asn	Leu	Asp	Asn	Tyr	Gly	Xaa
1					5						10		

(2) INFORMATION FOR SEQ ID NO: 75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(ix) Feature:

- (A) NAME/KEY: Other
- (B) LOCATION: 5
- (C) OTHER INFORMATION: Xaa is unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

Ala	Glu	Met	Lys	Xaa	Phe	Lys	Asn	Ala	Ile	Val	Gln	Glu	Ile	Asp
1					5					10				15

(2) INFORMATION FOR SEQ ID NO: 76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

192

(ii) MOLECULE TYPE: None

(ix) FEATURE:

(A) NAME/KEY: Other
(B) LOCATION: 3...3
(D) OTHER INFORMATION: Ala is Ala or Gln

(A) NAME/KEY: Other
(B) LOCATION: 7...7
(D) OTHER INFORMATION: Thr is Gly or Thr

(ix) Feature:

(A) NAME/KEY: Other
(B) LOCATION: 11
(C) OTHER INFORMATION: Xaa is unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

Val Ile Ala Gly Met Val Thr His Ile His Xaa Val Ala Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO: 77:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide
(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

Thr Asn Ile Val Val Leu Ile Lys Gln Val Pro Asp Thr Trp Ser
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 78:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide
(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

Ala Ile Gln Val Ser Val Leu Arg Val Phe Thr Asp Ser Asp Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 79:

193

(4) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

121 MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

{x} SEQUENCE DESCRIPTION: SEQ ID NO: 79:

Ala Lys Leu Ser Thr Asp Glu Leu Leu Asp Ala Phe Lys Glu Met
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 86:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(1) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

(ix) **FEATURE :**

- (A) NAME/KEY: Other
(B) LOCATION: 4...4
(D) OTHER INFORMATION: Asp is Asp of Gls

{xi} SEQUENCE DESCRIPTION: SEQ ID NO: 80:

Asp Pro Ala Asp Ala Pro Asp Val Pro Thr Ala Ala Gln Leu Thr
1 5 10 15

INFORMATION FOR GEO ID NO.: 84:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
(B) TYPR: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(11) MOLECULE TYPE: peptide

(v) **FRAGMENT TYPE:** N-terminal

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

Ala Glu Asp Val Arg Ala Glu Ile Val Ala Ser Val Leu Glu Val Val
1 5 10 15

Val Asn Glu Gly Asp Gln Ile Asp Lys Gly Asp Val Val Val Leu Leu
30 35 36

Glu Ser Met Tyr Met Glu Ile Pro Val Leu Ala Glu Ala Ala Gly Thr
35 40 45
Val Ser

(2) INFORMATION FOR SEQ ID NO: 82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

Thr	Thr	Ser	Pro	Asp	Pro	Tyr	Ala	Ala	Leu	Pro	Lys	Leu	Pro	Ser
1				5					10					15

(2) INFORMATION FOR SEQ ID NO: 83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

Thr	Glu	Tyr	Glu	Gly	Pro	Lys	Thr	Lys	Phe	His	Ala	Leu	Met	Gln
1				5					10					15

(2) INFORMATION FOR SEQ ID NO: 84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

Thr	Thr	Ile	Val	Ala	Leu	Lys	Tyr	Pro	Gly	Gly	Val	Val	Met	Ala
1				5					10					15

(2) INFORMATION FOR SEQ ID NO: 85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

195

(ii) MOLECULE TYPE: peptide
 (v) FRAGMENT TYPE: N-terminal
 (ix) FEATURE:
 (A) NAME/KEY: Other
 (B) LOCATION: 10
 (D) OTHER INFORMATION: Xaa is unknown

(ix) FEATURE:
 (A) NAME/KEY: Other
 (B) LOCATION: 15
 (D) OTHER INFORMATION: Xaa is unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

Ser	Phe	Pro	Tyr	Phe	Ile	Ser	Pro	Glu	Xaa	Ala	Met	Arg	Glu	Xaa
1				5					10				15	

(2) INFORMATION FOR SEQ ID NO: 86:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide
 (v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

Thr	His	Tyr	Asp	Val	Val	Val	Leu	Gly	Ala	Gly	Pro	Gly	Gly	Tyr
1				5				10					15	

(2) INFORMATION FOR SEQ ID NO: 87:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 450 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
 (B) LOCATION: 187...400
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

AGCCCGGTAA	TGAGTTCCGG	GCAATGCTGA	CCATCGGGTT	TGTTTCGGC	TATAACCGAA	60
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CGGTTTGTGT	ACGGGATACA	AATACGGGA	GGGAAGAAGT	AGGCAA	ATG	GAA	AAA	115
					Met	Glu	Lys	

1

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ATG TCA CAT GAT CCG ATC GCT GGC GAC ATT GGC ACG CAA GTG AGC GAC      163
Met Ser His Asp Pro Ile Ala Ala Asp Ile Gly Thr Gln Val Ser Asp
      5              10              15

AAC GCT CTG CAC GGC GTG ACG GCC GGC TGG ACG GCG CTG ACG TCG GTG      211
Asn Ala Leu His Gly Val Thr Ala Gly Ser Thr Ala Leu Thr Ser Val
      20              25              30              35

ACC GGG CTG GTT CCG GCG GGG GCC GAT GAG GTC TCC GCC CAA GCG GCG      259
Thr Gly Leu Val Pro Ala Gly Ala Asp Glu Val Ser Ala Gln Ala Ala
      40              45              50

ACG GCG TTC ACA TCG GAG GGC ATC CAA TTG CTG GCT TCC AAT GCA TCG      297
Thr Ala Phe Thr Ser Gln Gly Ile Gln Leu Leu Ala Ser Asn Ala Ser
      55              60              65

GCC CAA GAC CAG CTC CAC CGT GCG GGC GAA GCG GTC CAG GAC GTC GCC      355
Ala Gln Asp Gln Leu His Arg Ala Gly Glu Ala Val Gln Asp Val Ala
      70              75              80

CGC ACC TAT TCG CAA ATC GAC GAC GGC GCC GCC GGC GTC TTC GCC TAATA      495
Arg Thr Tyr Ser Gln Ile Asp Asp Gly Ala Ala Gly Val Phe Ala
      85              90              95

GGCCCCCAGC ACATCGGAGG GAGTGTATCAC CATGCTGTGG CACGC      450

```

(2) INFORMATION FOR SEQ ID NO: 88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

```

Met Glu Lys Met Ser His Asp Pro Ile Ala Ala Asp Ile Gly Thr Gln
 1              5              10              15

Val Ser Asp Asn Ala Leu His Gly Val Thr Ala Gly Ser Thr Ala Leu
20              25              30

Thr Ser Val Thr Gly Leu Val Pro Ala Gly Ala Asp Glu Val Ser Ala
35              40              45

Gln Ala Ala Thr Ala Phe Thr Ser Glu Gly Ile Gln Leu Leu Ala Ser
50              55              60

Asn Ala Ser Ala Gln Asp Gln Leu His Arg Ala Gly Glu Ala Val Gln
65              70              75              80

Asp Val Ala Arg Thr Tyr Ser Gln Ile Asp Asp Gly Ala Ala Gly Val
85              90              95

Phe Ala

```

(2) INFORMATION FOR SEQ ID NO: 89:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 468 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 37...453
 (C) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

GCAACCGGCT TTTCGATCAG CTGAGACATC AGCGGC GTG CGG GTC AAC GAC CCA	54
Met Arg Val Asn Asp Pro	
1 5	
CCT GCG CCA GGT AGC GAC TCC GCG CGC AGC AGG CCC GCG CCC GCG CTG	102
Pro Ala Pro Gly Ser Asp Ser Ala Arg Ser Arg Pro Ala Pro Ala Leu	
10 15 20	
GGG CCT GAT CCA CCA GCC AGC GGA TGG TTC GAC AGC GGA CTG GTG CCG	150
Gly Pro Asp Pro Pro Ala Ser Gly Trp Phe Asp Ser Gly Leu Val Pro	
25 30 35	
AGC AGG CCC ATC TGC GCG GCT TCC TCG TCG GCT GGG TTG CCG CCG CCG	198
Ser Arg Pro Ile Cys Ala Ala Ser Ser Ser Ala Gly Leu Pro Pro Pro	
40 45 50	
GTG CCG CCC ACC TGG CTG AAC AAC GAC GTC ACC TGC TGC AGC GGC TGG	246
Val Pro Pro Thr Trp Leu Asn Asn Asp Val Thr Cys Cys Ser Gly Trp	
55 60 65 70	
GTC AGC TGC TGC ATC GGG CCG CTC ATC TCA CCC AGT TGG CCG AGG GTC	294
Val Ser Cys Cys Ile Gly Pro Leu Ile Ser Pro Ser Trp Pro Arg Val	
75 80 85	
TGG GTA GCC GCC GGC GGC AAC TGG CCA ACC GGT GTT GAG CTG CCA GGG	342
Trp Val Ala Ala Gly Gly Asn Trp Pro Thr Gly Val Glu Leu Pro Gly	
90 95 100	
GAG GGC ATT CCG AAG ATC GGG TTC GTC GTG CTC TGG CTC GCG CCG GGA	390
Glu Gly Ile Pro Lys Ile Gly Phe Val Val Leu Trp Leu Ala Pro Gly	
105 110 115	
TCA AGG ATC GAC GCC ATC GGC TCG AOC TTC TCG AAA AGC GTG TTA ACC	438
Ser Arg Ile Asp Ala Ile Gly Ser Ser Phe Ser Lys Ser Val Leu Thr	
120 125 130	
GCG GTC TCG GCG TGG TAGACCT	468
Ala Val Ser Ala Trp	
135	

(2) INFORMATION FOR SEQ ID NO: 90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

```

Met Arg Val Asn Asp Pro Pro Ala Pro Gly Ser Asp Ser Ala Arg Ser
 1           5           10           15

Arg Pro Ala Pro Ala Leu Gly Pro Asp Pro Pro Ala Ser Gly Trp Phe
          20           25           30

Asp Ser Gly Leu Val Pro Ser Arg Pro Ile Cys Ala Ala Ser Ser Ser
          35           40           45

Ala Gly Leu Pro Pro Pro Val Pro Pro Thr Trp Leu Asn Asn Asp Val
          50           55           60

Thr Cys Cys Ser Gly Trp Val Ser Cys Cys Ile Gly Pro Leu Ile Ser
          65           70           75           80

Pro Ser Trp Pro Arg Val Trp Val Ala Ala Gly Gly Asn Trp Pro Thr
          85           90           95

Gly Val Glu Leu Pro Gly Glu Gly Ile Pro Lys Ile Gly Phe Val Val
          100          105          110

Leu Trp Leu Ala Pro Gly Ser Arg Ile Asp Ala Ile Gly Ser Ser Phe
          115          120          125

Ser Lys Ser Val Leu Thr Ala Val Ser Ala Trp
          130          135

```

(2) INFORMATION FOR SEQ ID NO: 91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1280 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 28...1140
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

200

220	225	230	
TCG TTG TTC ACC CAG GTG GGC GGC ACC GGC GGC AAC CCA GCC GAC			774
Ser Leu Phe Ser Ser Val Gly Gly Thr Gly Gly Asn Pro Ala Asp			
235	240	245	
GAG GAA GCC GCG CAG ATG GGC CTG CTC GGC ACC AGT CCG CTG TCG AAC			822
Glu Glu Ala Ala Gln Met Gly Leu Leu Gly Thr Ser Pro Leu Ser Asn			
250	255	260	265
CAT CCG CTG GCT GGT GGA TCA GGC CCC AGC GCG GGC GCG GGC CTG CTG			870
His Pro Leu Ala Gly Gly Ser Gly Pro Ser Ala Gly Ala Gly Leu Leu			
270	275	280	
CGC GCG GAG TCG CTA CCT GGC GCA GGT GGG TGG TTG ACC CGC ACG CCG			918
Arg Ala Glu Ser Leu Pro Gly Ala Gly Gly Ser Leu Thr Arg Thr Pro			
285	290	295	
CTG ATG TCT CAG CTG ATC GAA AAG CCG GTT GCC CCC TCG GTG ATG CCG			966
Leu Met Ser Ser Gln Leu Ile Glu Lys Pro Val Ala Pro Ser Val Met Pro			
300	305	310	
GCG GCT GCT GCC GGA TCG TCG GCG ACG GGT GGC GCC GCT CCG GTG GGT			1014
Ala Ala Ala Ala Gly Ser Ser Ala Thr Gly Gly Ala Ala Pro Val Gly			
315	320	325	
GCG GGA GCG ATG GCC CAG GGT GCG CAA TCC GGC GGC TCC ACC AGG CCG			1062
Ala Gly Ala Met Gly Gln Gly Ala Gln Ser Gly Gly Ser Thr Arg Pro			
330	335	340	345
GGT CTG GTC GCG CCG GCA CCG CTC GCG CAG GAG CGT GAA GAA GAC GAC			1110
Gly Leu Val Ala Pro Ala Pro Leu Ala Gln Glu Arg Glu Glu Asp Asp			
350	355	360	
GAG GAC GAC TGG GAC GAA GAG GAC GAC TGG TGAGCTCCCG TAATGACAAC AGA			1163
Glu Asp Asp Trp Asp Glu Glu Asp Asp Trp			
365	370		
CTTCCCGGCC ACCCGGCCCG GAAGACTTGC CAACATT			1200

(2) INFORMATION FOR SEQ ID NO: 92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 371 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

Met Ile Thr Met Leu Trp His Ala Met Pro Pro Glu Leu Asn Thr Ala
 1 5 10 15

Arg Leu Met Ala Gly Ala Gly Pro Ala Pro Met Leu Ala Ala Ala Ala

201

20				25				30							
Gly	Trp	Gln	Thr	Leu	Ser	Ala	Ala	Leu	Asp	Ala	Gln	Ala	Val	Glu	Leu
	35						40						45		
Thr	Ala	Arg	Leu	Asn	Ser	Leu	Gly	Glu	Ala	Trp	Thr	Gly	Gly	Gly	Ser
	50				55						60				
Asp	Lys	Ala	Leu	Ala	Ala	Ala	Thr	Pro	Met	Val	Val	Trp	Leu	Gln	Thr
	65				70					75				80	
Ala	Ser	Thr	Gln	Ala	Lys	Thr	Arg	Ala	Met	Gln	Ala	Thr	Ala	Gln	Ala
			85						90					95	
Ala	Ala	Tyr	Thr	Gln	Ala	Met	Ala	Thr	Thr	Pro	Ser	Leu	Pro	Glu	Ile
			100				105							110	
Ala	Ala	Asn	His	Ile	Thr	Gln	Ala	Val	Leu	Thr	Ala	Thr	Asn	Phe	Phe
		115				120							125		
Gly	Ile	Asn	Thr	Ile	Pro	Ile	Ala	Leu	Thr	Glu	Met	Asp	Tyr	Phe	Ile
	130					135					140				
Arg	Met	Trp	Asn	Gln	Ala	Ala	Leu	Ala	Met	Glu	Val	Tyr	Gln	Ala	Glu
	145				150					155				160	
Thr	Ala	Val	Asn	Thr	Leu	Phe	Glu	Lys	Leu	Glu	Pro	Met	Ala	Ser	Ile
			165				170							175	
Leu	Asp	Pro	Gly	Ala	Ser	Gln	Ser	Thr	Thr	Asn	Pro	Ile	Phe	Gly	Met
	180						185							190	
Pro	Ser	Pro	Gly	Ser	Ser	Thr	Pro	Val	Gly	Gln	Leu	Pro	Pro	Ala	Ala
	195						200							205	
Thr	Gln	Thr	Leu	Gly	Gln	Leu	Gly	Glu	Met	Ser	Gly	Pro	Met	Gln	Gln
	210					215					220				
Leu	Thr	Gln	Pro	Leu	Gln	Gln	Val	Thr	Ser	Leu	Phe	Ser	Gln	Val	Gly
	225				230					235				240	
Gly	Thr	Gly	Gly	Gly	Asn	Pro	Ala	Asp	Glu	Glu	Ala	Ala	Gln	Met	Gly
			245						250					255	
Leu	Leu	Gly	Thr	Ser	Pro	Leu	Ser	Asn	His	Pro	Leu	Ala	Gly	Gly	Ser
		260					265							270	
Gly	Pro	Ser	Ala	Gly	Ala	Gly	Leu	Leu	Arg	Ala	Glu	Ser	Leu	Pro	Gly
	275						280							285	
Ala	Gly	Gly	Ser	Leu	Thr	Arg	Thr	Pro	Leu	Met	Ser	Gln	Leu	Ile	Glu
	290				295						300				
Lys	Pro	Val	Ala	Pro	Ser	Val	Met	Pro	Ala	Ala	Ala	Gly	Ser	Ser	
	305				310					315				320	
Ala	Thr	Gly	Gly	Ala	Ala	Pro	Val	Gly	Ala	Gly	Ala	Met	Gly	Gln	Gly
		325					330							335	

202

Ala Gln Ser Gly Gly Ser Thr Arg Pro Gly Leu Val Ala Pro Ala Pro
 340 345 350

Leu Ala Gln Glu Arg Glu Glu Asp Asp Glu Asp Asp Trp Asp Glu Glu
 355 360 365

Asp Asp Trp
 370

(2) INFORMATION FOR SEQ ID NO: 93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1000 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 46...969
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

GACGCGACAC AGAATCCTT AAGGCTGGCG GCCAAGGGCG CGAAG GTG AAG AAG GTG 57
 Met Lys Lys Val
 1

AAG CCC CAG AAA CCG AAG GCC ACG AAG CCG CCC AAA GTG GTG TCG CAG 105
 Lys Pro Gln Lys Pro Lys Ala Thr Lys Pro Pro Lys Val Val Ser Gln
 5 10 15 20

CGC GGC TGG CGA CAT TGG GTG CAT GCG TTG ACG CGA ATC AAC CTG GGC 153
 Arg Gly Trp Arg His Trp Val His Ala Leu Thr Arg Ile Asn Leu Gly
 25 30 35

CTG TCA CCC GAC GAG AAG TAC GAG CTG GAC CTG CAC GCT CGA GTC CCG 201
 Leu Ser Pro Asp Glu Lys Tyr Glu Leu Asp Leu His Ala Arg Val Arg
 40 45 50

CGC AAT CCC CGG GGG TCG TAT CAG ATC GCC GTC GTC GGT CTC AAA GGT 249
 Arg Asn Pro Arg Gly Ser Tyr Gln Ile Ala Val Val Gly Leu Lys Gly
 55 60 65

GGG GCT GGC AAA ACC ACG CTG ACA GCA GCG TTG GGG TCG ACC TTG GCT 297
 Gly Ala Gly Lys Thr Thr Leu Thr Ala Ala Leu Gly Ser Thr Leu Ala
 70 75 80

CAG GTG GGG GCC GAC CGG ATC CTG GCT CTA GAC GCG GAT CCA GGC GCC 345
 Gln Val Arg Ala Asp Arg Ile Leu Ala Leu Asp Ala Asp Pro Gly Ala
 85 90 95 100

GGA AAC CTC GCC GAT CCG GTA GGG CGA CAA TCG GGC GCG ACC ATC GCT 393
 Gly Asn Leu Ala Asp Arg Val Gly Arg Gln Ser Gly Ala Thr Ile Ala
 105 110 115

203

GAT GTG CTT GCA GAA AAA GAG CTG TCG CAC TAC AAC GAC ATC CGC GCA Asp Val Leu Ala Glu Lys Glu Leu Ser His Tyr Asn Asp Ile Arg Ala 120 125 130	441
CAC ACT AGC GTC AAT GCG GTC AAT CTG GAA GTG CTG CCG GCA CCG GAA His Thr Ser Val Asn Ala Val Asn Leu Glu Val Leu Pro Ala Pro Glu 135 140 145	449
TAC AGC TCG GCG CAG CGC CCG CTC AGC GAC GCC GAC TGG CAT TTC ATC Tyr Ser Ser Ala Gln Arg Ala Leu Ser Asp Ala Asp Trp His Phe Ile 150 155 160	537
GCC GAT CCT GCG TCG AGG TTT TAC AAC CTC GTC TTG GCT GAT TGT GGG Ala Asp Pro Ala Ser Arg Phe Tyr Asn Leu Val Leu Ala Asp Cys Gly 165 170 175 180	585
GCC GGC TTU TTC GAC CCG CTG ACC CGC GGC GTG CTG TCC ACG GTU TCC Ala Gly Phe Phe Asp Pro Leu Thr Arg Gly Val Leu Ser Thr Val Ser 185 190 195	633
GGT GTC GTG GTC GTG GCA AGT GTC TCA ATC GAC GGC GCA CAA CAG GCG Gly Val Val Val Val Ala Ser Val Ser Ile Asp Gly Ala Gln Gln Ala 200 205 210	681
TCG GTC GCG TTG GAC TGG TTG CGC AAC AAC GGT TAC CAA GAT TTG GCG Ser Val Ala Leu Asp Trp Leu Arg Asn Asn Gly Tyr Gln Asp Leu Ala 215 220 225	729
AGC CGC GCA TGC GTG GTC ATC AAT CAC ATC ATG CCG GGA GAA CCC AAT Ser Arg Ala Cys Val Val Ile Asn His Ile Met Pro Gly Glu Pro Asn 230 235 240	777
GTC GCA GTT AAA GAC CTG GTG CCG CAT TTC GAA CAG CAA GTT CAA CCC Val Ala Val Lys Asp Leu Val Arg His Phe Glu Gln Gln Val Gln Pro 245 250 255 260	825
GGC CGG GTC GTG GTC ATG CCG TGG GAC AGG CAC ATT GCG GCC GGA ACC Gly Arg Val Val Val Met Pro Trp Asp Arg His Ile Ala Ala Gly Thr 265 270 275	873
GAG ATT TCA CTC GAC TTG CTC GAC CCT ATC TAC AAG CGC AAG GTC CTC Glu Ile Ser Leu Asp Leu Leu Asp Pro Ile Tyr Lys Arg Lys Val Leu 280 285 290	921
GAA TTG GCC GCA GCG CTA TCC GAC GAT TTC GAG AGG GCT GGA CGT CGT T Glu Leu Ala Ala Ala Leu Ser Asp Asp Phe Glu Arg Ala Gly Arg Arg 295 300 305	970
GAGCCGACCT GCTGTGCTG CTGGTCTAC	1000

(2) INFORMATION FOR SEQ ID NO: 94:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 308 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(x) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

Met	Lys	Lys	Val	Lys	Pro	Gln	Lys	Pro	Lys	Ala	Thr	Lys	Pro	Lys	
1				5					10					15	
Val	Val	Ser	Gln	Arg	Gly	Trp	Arg	His	Trp	Val	His	Ala	Leu	Thr	Arg
			20				25						30		
Ile	Asn	Leu	Gly	Leu	Ser	Pro	Asp	Glu	Lys	Tyr	Glu	Leu	Asp	Leu	His
		35					40					45			
Ala	Arg	Val	Arg	Arg	Asn	Pro	Arg	Gly	Ser	Tyr	Gln	Ile	Ala	Val	Val
		50			55						60				
Gly	Leu	Lys	Gly	Gly	Ala	Gly	Lys	Thr	Thr	Leu	Thr	Ala	Ala	Leu	Gly
65					70				75					80	
Ser	Thr	Leu	Ala	Glu	Val	Arg	Ala	Asp	Arg	Ile	Leu	Ala	Leu	Asp	Ala
				85				90						95	
Asp	Pro	Gly	Ala	Gly	Asn	Leu	Ala	Asp	Arg	Val	Gly	Arg	Gln	Ser	Gly
		100						105					110		
Ala	Thr	Ile	Ala	Asp	Val	Leu	Ala	Glu	Lys	Glu	Leu	Ser	His	Tyr	Asn
		115				120							125		
Asp	Ile	Arg	Ala	His	Thr	Ser	Val	Asn	Ala	Val	Asn	Leu	Glu	Val	Leu
	130				135						140				
Pro	Ala	Pro	Glu	Tyr	Ser	Ser	Ala	Gln	Arg	Ala	Leu	Ser	Asp	Ala	Asp
145				150					155					160	
Trp	His	Phe	Ile	Ala	Asp	Pro	Ala	Ser	Arg	Phe	Tyr	Asn	Leu	Val	Leu
		165						170					175		
Ala	Asp	Cys	Gly	Ala	Gly	Phe	Phe	Asp	Pro	Leu	Thr	Arg	Gly	Val	Leu
		180				185							190		
Ser	Thr	Val	Ser	Gly	Val	Val	Val	Val	Ala	Ser	Val	Ser	Ile	Asp	Gly
	195				200							205			
Ala	Gln	Gln	Ala	Ser	Val	Ala	Leu	Asp	Trp	Leu	Arg	Asn	Asn	Gly	Tyr
	210				215					220					
Gln	Asp	Leu	Ala	Ser	Arg	Ala	Cys	Val	Val	Ile	Asn	His	Ile	Met	Pro
225				230					235					240	
Gly	Glu	Pro	Asn	Val	Ala	Val	Lys	Asp	Leu	Val	Arg	His	Phe	Glu	Gln
		245					250						255		
Gln	Val	Gln	Pro	Gly	Arg	Val	Val	Val	Met	Pro	Trp	Asp	Arg	His	Ile
	260				265							270			
Ala	Ala	Gly	Thr	Glu	Ile	Ser	Leu	Asp	Leu	Leu	Asp	Pro	Ile	Tyr	Lys
	275				280							285			